

Fig. 1

200bp

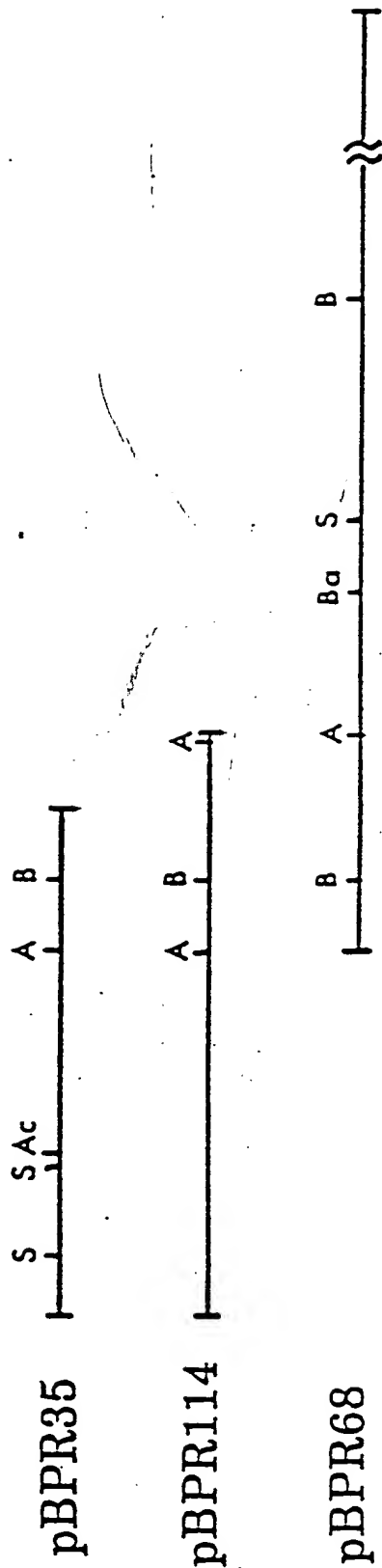


Fig. 2

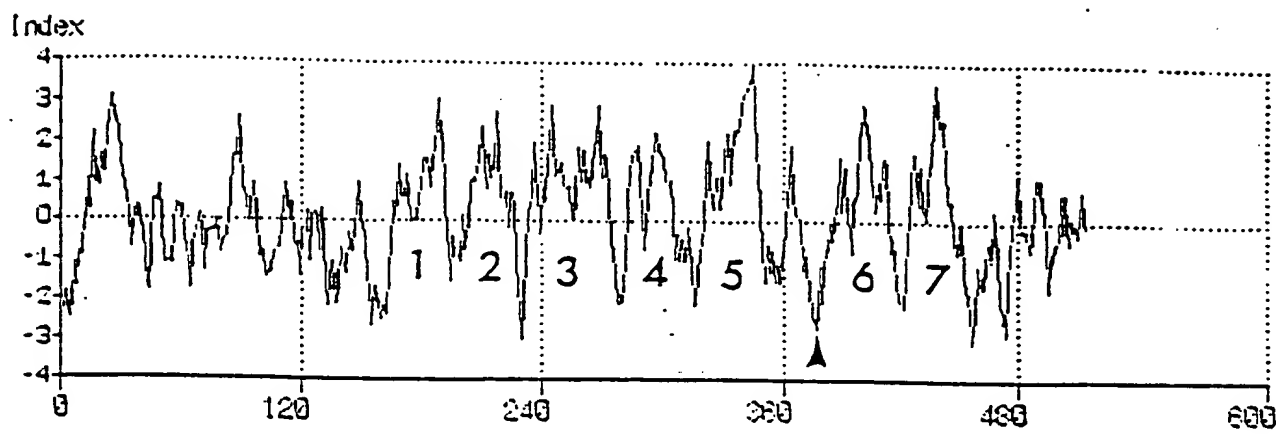
1	TGGCCTGCACCCACCCCAACCTGCGGAAGACGGGGGAGCGCGTGGTGGTGGCTCCCTCCTGCCCTGGGCTGGCTTCCGGTGGAG	91
92	GGCGTGCCTCTCCGGCAAGCCAGACCAGGCTGGGGGACCGCGGGCGGGCGGCTAGGGAAGCCGGGGGCTCCCGCTGGGGCCCGG	183
184	GGCGGACTGACAGCGCGCGGGGGGGGGGAGCGGCTCCAAAGCGGAGCGTGCTCCCGCGTGGGCACAAGCTGGCGCGCGCGGAGGACCCA	273
278	CGGACACCGCGCGCGGGGGGACACACAGACCGGGAGATCGGGCTCTACCGCGGCTACTCAGCGGACGAGTCCCCATCCCTGGCGGGAGCGG	367
388	GGCGGCGACTCGCGGCTGGCGGCGCTCCCGCGGAGTCTGCCCGGGGACACCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGGAGGCGGCTGGTGAGCA	459
1		
460	GCCTGTAGACACCTGGGTTGAGCAGTGGCGGCTGTGA	13
	Met Arg Gly Gly Arg His Trp Pro Glu Pro Pro Cys Arg	536
	ATG AGA GCG GGG GCG CAC TGG CCC GAG CCG CCG TGC AGG	
14	Leu Arg Ser Val Met Ala Ser Ile Ala Gln Val Ser Leu Ala Ala Leu Leu Leu Leu Pro Met Ala Thr	36
537	CTG AGA AGC GTC ATG GCC AGC ATC GCG CAG GTC TCC CTG GCT GCT CTC CTC CTG CTG CCT ATG GCC ACC	605
37	Ala Met His Ser Asp Cys Ile Phe Lys Lys Glu Gln Ala Met Cys Leu Glu Lys Ile Gln Arg Val Asn	59
506	GCG ATG CAT TCC GAG TGC ATC TTC AAG AAG GAG CAA GCC ATG TGC CTG GAG AAG ATC CAG AGG GTC AAT	674
60	Asp Leu Met Gly Leu Asn Asp Ser Ser Pro Gly Cys Pro Gly Met Trp Asp Asn Ile Thr Cys Trp Lys	82
675	GAC CTG ATG GCG TTG AAT GAC TCC TCC CCA GGG TGC CCT GGG ATG TGG GAC AAC ATC ACG TGT TGG AAG	743
83	Pro Ala His Val Gly Glu Met Val Leu Val Ser Cys Pro Glu Leu Phe Arg Ile Phe Asn Pro Asp Gln	105
744	CCC GCC CAC GTG GGT GAG ATG GTC GTG GTC AGT TCC CCT GAA CTC TTC CCA ATC TTC AAC CCA GAC CAA	812
106	Val Trp Glu Thr Glu Thr Ile Gly Glu Phe Gly Phe Ala Asp Ser Lys Ser Leu Asp Leu Ser Asp Met	128
813	GTC TGG GAG ACG GAA ACC ATC GGA GAG TTC GGT TTT GCA GAC AGT AAA TCC TTG GAT CTC TCA GAC ATG	881
129	Arg Val Val Ser Arg Asn Cys Thr Glu Asp Gly Trp Ser Glu Pro Phe Pro His Tyr Phe Asp Ala Cys	151
882	AGG GTG GTG AGC CGG AAT TCC ACC GAG GAT GGA TGG TCA GAG CCA TTC CCT CAT TAT TTC GAT GCC TGT	950
152	Gly Phe Glu Glu Tyr Glu Ser Glu Thr Gly Asp Gln Asp Tyr Tyr Tyr Leu Ser Val Lys Ala Leu Tyr	174
951	GGG TTT GAG GAG TAC GAA TCT GAG ACT GCG GAG CAG GAT TAC TAC TAC CTC TCA GTG AAG GCC CTG TAC	1019
175	Thr Val Gly Tyr Ser Thr Ser Leu Val Thr Leu Thr Thr Ala Met Val Ile Leu Cys Arg Phe Arg Lys	197
1020	ACA GTT GGC TAC AGC ACC TCC CTC GTC ACC CTC ACC ACT GCC ATG GTC ATC CTG TGT CGT TTC CGG AAG	1088
198	Leu His Cys Thr Arg Asn Phe Ile His Met Asn Leu Phe Val Ser Phe Met Leu Arg Ala Ile Ser Val	220
1089	CTG CAC TGC ACC CGC AAC TTC ATC CAC ATC AAC CTC TTC GTG TCG TTT ATG CTG AGG GCC ATC TCC GTC	1157
221	Phe Ile Lys Asp Trp Ile Leu Tyr Ala Glu Gln Asp Ser Asn His Cys Phe Val Ser Thr Val Glu Cys	243
1158	TTC ATC AAA GAC TGG ATC CTC TAT GCT GAG CAG GAC AGC AAT CAC TGC TTT GTC TCC ACT GTG GAA TGC	1226
244	Lys Ala Val Met Val Phe Phe His Tyr Cys Val Val Ser Asn Tyr Phe Trp Leu Phe Ile Glu Gly Leu	266
1227	AAG GCT GTG ATG GTT TTC TTC CAC TAC TGT GTT GTA TCC AAC TAC TTC TGG CTG TTC ATC GAG GGC CTG	1295
267	Tyr Leu Phe Thr Leu Leu Val Glu Thr Phe Phe Pro Glu Arg Arg Tyr Phe Tyr Trp Tyr Ile Ile Ile	289
1296	TAT CTC TTC ACC CTG CTG GTC GAG ACC TTC TTC CCC GAG AGG AGA TAT TTC TAC TGG TAC ATC ATT	1364
290	Gly Trp Gly Thr Pro Thr Val Cys Val Ser Val Trp Ala Met Leu Arg Leu Tyr Phe Asp Asp Thr Gly	312
1365	GGC TGG GGG ACA CCA ACT GTG TGT GTG TCT GTG TGG GCT ATG CTG AGG CTC TAC TTC GAT GAC ACA GGC	1433
313	Cys Trp Asp Met Asn Asp Asn Thr Ala Leu Trp Trp Val Ile Lys Gly Pro Val Val Gly Ser Ile Met	335
1434	TGC TGG GAT ATG AAT GAC AAC ACG GCT CTG TGG TGG GTG ATC AAA GGC CCT GTA GTT GGC TCC ATA ATG	1502
336	Val Asn Phe Val Leu Phe Ile Gly Ile Ile Val Ile Leu Val Gln Lys Leu Gln Ser Pro Asp Met Gly	358
1503	GTT AAT TTT GTG CTC TTC ATC GGC ATC ATT GTC ATC GTT GTG CAG AAA CTT CAG TCT CCA GAC ATG GGA	1571
359	Gly Asn Glu Ser Ser Ile Tyr Phe Ser Cys Val Gln Lys Cys Tyr Cys Lys Pro Gln Arg Ala Gln Gln	381
1572	GGC AAC GAG TCC AGC ATC TAC TTC AGC TGC GTG CAG AAA TGC TAC TGC AAG CCA CAG CGG GCT CAG CAG	1640
382	His Ser Cys Lys Met Ser Glu Leu Ser Thr Ile Thr Leu Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile	404
1841	CAC TCT TGC AAG ATG TCA GAA CTG TCC ACC ATT ACT CTA CGG CTC GCC AGG TCC ACC TTG CTG CTC ATC	1709
405	Pro Leu Phe Gly Ile His Tyr Thr Val Phe Ala Phe Ser Pro Glu Asn Val Ser Lys Arg Glu Arg Leu	427
1710	CCA CTC TTT GGA ATC CAC TAC ACT GTC TTT GCT TTC TCC CCG GAG AAC GTC ACC AAG AGG CAG ACA CTG	1778
428	Val Phe Glu Leu Gly Leu Gly Ser Phe Gln Gly Phe Val Val Ala Val Leu Tyr Cys Phe Leu Asn Gly	450
1779	GTG TTT GAG CTG GGT CTG GGC TCC TTC CAG GGC TTT GTG CTG GCT GTT CTC TAT TGC TTT CTG AAT GGA	1847
451	Glu Val Gln Ala Glu Ile Lys Arg Lys Trp Arg Ser Trp Lys Val Asn Arg Tyr Phe Thr Met Asp Phe	473
1848	GAG GTG CAG GCG GAG ATC AAG AGG AAG TGC CGG AGC TGG AAG GTG AAC CCG TAC TTC ACC ATG GAC TTC	1916
474	Lys His Arg His Pro Ser Leu Ala Ser Ser Gly Val Asn Gly Gly Thr Gln Leu Ser Ile Leu Ser Lys	496
1917	AAG CAC CGG CAC CCA TCC CTG GCC AGC AGC GGG GTG AAC GGG GGC ACC CAG CTC TCC ATC CTG AGC AAG	1985
497	Ser Ser Ser Gln Ile Arg Met Ser Gly Leu Pro Ala Asp Asn Leu Ala Thr	513
1986	AGC AGC TCC CAG ATC CGC ATG TCT GGG CTT CCG GCC GAC AAC CTG GCC ACC TGA GCCACCGCTCCCCCTCCTC	2059
2060	TCCTCTGTACCGAGGCTGGCGCTGTGTCGGGGGGGGGGCCAGCATGTTGTGCTCTTCTCGGCTTGGGCGAGGCGCGGCTGGGCGCT	2151
2152	GGCCCCCGAGGTTGGAGAAGCATCGCGCACCGCAGCTGTTTACGCTTCTGTTTGGCGCTGGCCCAACCGTGGTCCCTGGGCGCTGC	2243
2244	ACCCAGACATGTAATACTCCTTAATTGGGAAGTCATCCATTCTTCCCTTTCCCAAGTCCTTGCTTATTAAGAGTTCAAGTCACCTACCCA	2335
2336	ATTGACAAGCTTAAGTAACCACTAACCACCGTCACTCGTGGGAGGCTCCCATGGGCTGAGCTACTGACTTGGCTTTGGGGGCTTGGGCT	2427
2428	GGGGCGCTCCTTAAAGCCCCCTGAAATTGTGGACCTCAAAGTGTGACTCTTTGAGTCTACTCGCCACCGCGTGGCGCTTTCAGCGCC	2519
2520	TGGTCCAGTCACCGAGGTTACTGCAAGTCCAGCTTGGATGGCCAGACAGCTTTTGGCACAGGACAGCCATGCTCACCAACATTTTACTG	2611
2612	TCCAGGTGCCAGGTGCCAGGTGCCAGCTCCTGGGCATCAGACAGTGGGAAAGCTCCAGGATCTACCATTCAGAGACTTCAGTTTGGAT	2703
2704	GTAGGGCTAAGCCACAGAAAAAGTTCTGGAGCTTTTCATTTGGCCCAAGAAAAAGTCCCAAGATCCAGAAAAAGTGGATCTGAGTGGAAATT	2795
2796	AGATGCAAGAGCTTGGAG	2814

000259410000004

[illegible]

Fig. 5

A



B

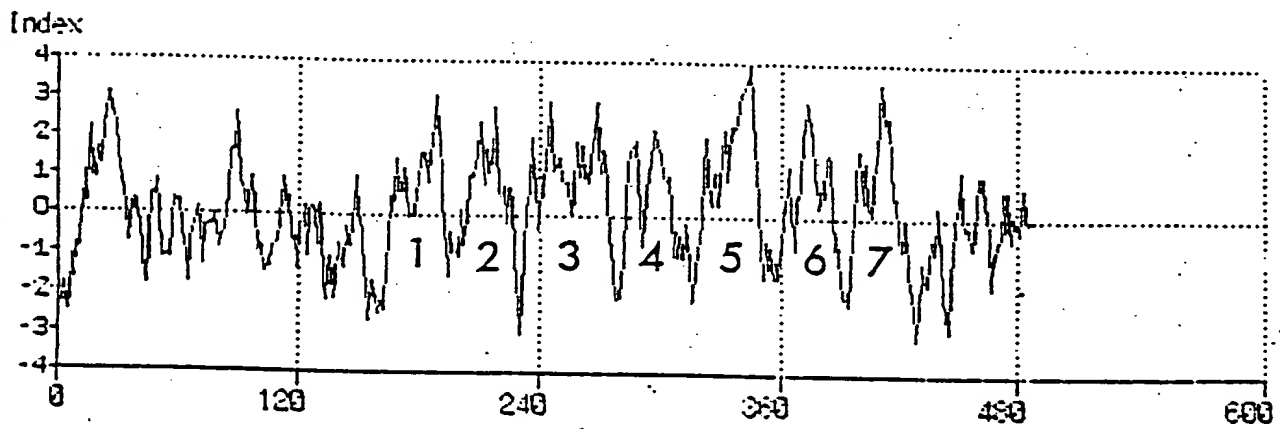


Fig. 6

100 bp

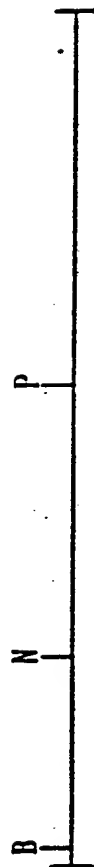
pRPACAPR 18



pRPACAPR 46



pRPACAPR 5



pRPACAPR 12



Fig. 7

1	CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA	58
59	TAGTGGCTGGGAAGCACCATGGCCAGAGTCTTGCAGCTCTCCCTGACTGCTCTCCTGCTG	118
1	MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu	14
119	CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG	178
15	ProValAlaIleAlaMethHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu	34
179	GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT	238
35	GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro	54
239	GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA	298
55	GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal	74
299	AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA	358
75	SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle	94
359	GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGAGATCACAGACATGGGGGTCGTGGGC	418
95	GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly	114
419	CGGAAGTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG	478
115	ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly	134
479	TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT	538
135	PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla	154
539	CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG	598
155	LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu	174
599	TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC	658
175	CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer	194
659	TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC	718
195	PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp	214
719	AGCAGTCACTGCTTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC	778
215	SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr	234
779	TGCGTGGTGTCCAAGTCTTCTGGCTGTTTCAATTGAAGGCCTGTACCTCTTTACACTGCTG	838
235	CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu	254
839	GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG	898
255	ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly	274
899	ACACCTACTGTGTGTGTAAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA	958
275	ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly	294
959	TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCCGTGGTTGGC	1018
295	CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly	314
1019	TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCCTTGTACAGAAGCTG	1078
315	SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu	334
1079	CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTACGGCTGGCCCGCTCCACC	1138
335	GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrLeuArgLeuAlaArgSerThr	354

Fig. 8

1139 CTACTGCTCATCCCACTCTTCGGAATCCACTACACAGTATTCGCCTTCTCTCCAGAGAAC 1198
 355 LeuLeuLeuIleProLeuPheGlyIleHisTyrThrValPheAlaPheSerProGluAsn 374

1199 GTCAGCAAGAGGGGAAAGACTTGTGTTTGAGCTTGGGCTGGGCTCCTTCCAGGGCTTTGTG 1258
 375 ValSerLysArgGluArgLeuValPheGluLeuGlyLeuGlySerPheGlnGlyPheVal 394

1259 GTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTACAGGCAGAGATTAAGAGGAAATGG 1318
 395 ValAlaValLeuTyrCysPheLeuAsnGlyGluValGlnAlaGluIleLysArgLysTrp 414

1319 AGGAGCTGGAAGGTGAACCGTTACTTCACTATGGACTTCAAGCACCGGCACCCGTCCCTG 1378
 415 ArgSerTrpLysValAsnArgTyrPheThrMetAspPheLysHisArgHisProSerLeu 434

1379 GCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCCATCCTGAGCAAGAGCAGCTCCAG 1438
 435 AlaSerSerGlyValAsnGlyGlyThrGlnLeuSerIleLeuSerLysSerSerSerGln 454

1439 CTCCGCATGTCCAGCCTCCCGGCCGACAACTTGGCCACCTGAGGCCTGTCTCCCTCCTCC 1498
 455 LeuArgMetSerSerLeuProAlaAspAsnLeuAlaThr*** 467

1499 TTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAGCATGTTTGTGCCTCTCCCCTCTCC 1558
 1559 TTGGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCCCAAAGGGGAAGAGAGAGATAGGGT 1618
 1619 ATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACCTACTGTGATTTCATTGAGCCTGATT 1678
 1679 TGACATGTAAATACACCTCAAATTTGGAAAGTTGCCCCATCTCTGCCCCCAACCCATGCC 1738
 1739 CCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACTGTGTCAAGGCCAGCCTCAGTGATA 1798
 1799 GTCTGATCCCAGGTACAAGGCCTTGTGAGCTGAGGCTGAAAGGCCTGTTTGGAGAGGCT 1858
 1859 GGGGTAGTGCC 1869

Fig. 9

1	CGAGTGGACAGTGGCAGGCGGTGACTGAATCTCCAAGTCTGGAAACAATAGCCAGAGA	58
59	TAGTGGCTGGGAAGCACCATGGCCAGAGTCCTGCAGCTCTCCCTGACTGCTCTCCTGCTG	118
1	MetAlaArgValLeuGlnLeuSerLeuThrAlaLeuLeuLeu	14
119	CCTGTGGCTATTGCTATGCACTCTGACTGCATCTTCAAGAAGGAGCAAGCCATGTGCCTG	178
15	ProValAlaIleAlaMetHisSerAspCysIlePheLysLysGluGlnAlaMetCysLeu	34
179	GAGAGGATCCAGAGGGCCAACGACCTGATGGGACTAAACGAGTCTTCCCCAGGTTGCCCT	238
35	GluArgIleGlnArgAlaAsnAspLeuMetGlyLeuAsnGluSerSerProGlyCysPro	54
239	GGCATGTGGGACAATATCACATGTTGGAAGCCAGCTCAAGTAGGTGAGATGGTCCTTGTA	298
55	GlyMetTrpAspAsnIleThrCysTrpLysProAlaGlnValGlyGluMetValLeuVal	74
299	AGCTGCCCTGAGGTCTTCCGGATCTTCAACCCGGACCAAGTCTGGATGACAGAAACCATA	358
75	SerCysProGluValPheArgIlePheAsnProAspGlnValTrpMetThrGluThrIle	94
359	GGAGATTCTGGTTTTGCCGATAGTAATTCCTTGGAGATCACAGACATGGGGGTCGTGGGC	418
95	GlyAspSerGlyPheAlaAspSerAsnSerLeuGluIleThrAspMetGlyValValGly	114
419	CGGAAGTGCACAGAGGACGGCTGGTCGGAGCCCTTCCCCCACTACTTCGATGCTTGTGGG	478
115	ArgAsnCysThrGluAspGlyTrpSerGluProPheProHisTyrPheAspAlaCysGly	134
479	TTTGATGATTATGAGCCTGAGTCTGGAGATCAGGATTATTACTACCTGTCGGTGAAGGCT	538
135	PheAspAspTyrGluProGluSerGlyAspGlnAspTyrTyrTyrLeuSerValLysAla	154
539	CTCTACACAGTCGGCTACAGCACTTCCCTCGCCACCCTCACTACTGCCATGGTCATCTTG	598
155	LeuTyrThrValGlyTyrSerThrSerLeuAlaThrLeuThrThrAlaMetValIleLeu	174
599	TGCCGCTTCCGGAAGCTGCATTGCACTCGCAACTTCATCCACATGAACCTGTTTGTATCC	658
175	CysArgPheArgLysLeuHisCysThrArgAsnPheIleHisMetAsnLeuPheValSer	194
659	TTCATGCTGAGGGCTATCTCCGTCTTCATCAAGGACTGGATCTTGTACGCCGAGCAGGAC	718
195	PheMetLeuArgAlaIleSerValPheIleLysAspTrpIleLeuTyrAlaGluGlnAsp	214
719	AGCAGTCACTGCTTCGTTTCCACCGTGGAGTGCAAAGCTGTCATGGTTTTCTTCCACTAC	778
215	SerSerHisCysPheValSerThrValGluCysLysAlaValMetValPhePheHisTyr	234
779	TGCGTGGTGTCCAAGTACTTCTGGCTGTTTCATTGAAGGCCTGTACCTCTTTACTGCTG	838
235	CysValValSerAsnTyrPheTrpLeuPheIleGluGlyLeuTyrLeuPheThrLeuLeu	254
839	GTGGAGACCTTCTTCCCTGAGAGGAGATATTTCTACTGGTACACCATCATCGGCTGGGGG	898
255	ValGluThrPhePheProGluArgArgTyrPheTyrTrpTyrThrIleIleGlyTrpGly	274
899	ACACCTACTGTGTGTGTAACAGTGTGGGCTGTGCTGAGGCTCTATTTTGATGATGCAGGA	958
275	ThrProThrValCysValThrValTrpAlaValLeuArgLeuTyrPheAspAspAlaGly	294
959	TGCTGGGATATGAATGACAGCACAGCTCTGTGGTGGGTGATCAAAGGCCCGTGTTGGC	1018
295	CysTrpAspMetAsnAspSerThrAlaLeuTrpTrpValIleLysGlyProValValGly	314
1019	TCTATAATGGTTAACTTTGTGCTTTTCATCGGCATCATCATCCTTGTACAGAAGCTG	1078
315	SerIleMetValAsnPheValLeuPheIleGlyIleIleIleIleLeuValGlnLysLeu	334
1079	CAGTCCCCAGACATGGGAGGCAACGAGTCCAGCATCTACTTCAGCTGCGTGCAGAAATGC	1138
335	GlnSerProAspMetGlyGlyAsnGluSerSerIleTyrPheSerCysValGlnLysCys	354

Fig. 10

1139 TACTGCAAGCCACAGCGGGCTCAGCAGCACTCTTGCAAGATGTCAGAACTATCCACCATT 1198
 355 TyrCysLysProGlnArgAlaGlnGlnHisSerCysLysMetSerGluLeuSerThrIle 374

1199 ACTCTACGGCTGGCCCCGCTCCACCCTACTGCTCATCCCACTCTTCGGAATCCACTACACA 1258
 375 ThrLeuArgLeuAlaArgSerThrLeuLeuLeuIleProLeuPheGlyIleHisTyrThr 394
 △

1259 GTATTTCGCCTTCTCTCCAGAGAACGTCAGCAAGAGGGAAAGACTTGTGTTTGAGCTTGGG 1318
 395 ValPheAlaPheSerProGluAsnValSerLysArgGluArgLeuValPheGluLeuGly 414

1319 CTGGGCTCCTTCCAGGGCTTTGTGGTGGCTGTACTCTACTGCTTCCTGAATGGGGAGGTA 1378
 415 LeuGlySerPheGlnGlyPheValValAlaValLeuTyrCysPheLeuAsnGlyGluVal 434

1379 CAGGCAGAGATTAAGAGGAAATGGAGGAGCTGGAAGGTGAACCGTTACTTCACTATGGAC 1438
 435 GlnAlaGluIleLysArgLysTrpArgSerTrpLysValAsnArgTyrPheThrMetAsp 454

1439 TTCAAGCACCGGCACCCGTCCCTGGCCAGCAGTGGAGTAAATGGGGGAACCCAGCTGTCC 1498
 455 PheLysHisArgHisProSerLeuAlaSerSerGlyValAsnGlyGlyThrGlnLeuSer 474

1499 ATCCTGAGCAAGAGCAGCTCCAGCTCCGCATGTCCAGCCTCCCGGCCGACAACCTTGGCC 1558
 475 IleLeuSerLysSerSerSerGlnLeuArgMetSerSerLeuProAlaAspAsnLeuAla 494

1559 ACCTGAGGCCTGTCTCCCTCCTCCTTCTGCACAGGCTGGGGCTGCGGGCCAGTGCCTGAG 1618
 495 Thr*** 495

1619 CATGTTTGTGCCTCTCCCCCTCTCCTTGGGCAGGCCCTGGGTAGGAAGCTGGGCTCCTCCC 1678
 1679 CAAAGGGGAAGAGAGAGATAGGGTATAGGCTGATATTGCTCCTCCTGTTTGGGTCCCACC 1738
 1739 TACTGTGATTTCATTGAGCCTGATTTGACATGTAAATACACCTCAAATTTGGAAAGTTGCC 1798
 1799 CCATCTCTGCCCCCAACCCATGCCCCCTGCTCACCTCTGCCAGGCCCCAGCTCAACCTACT 1858
 1859 GTGTCAAGGCCAGCCTCAGTGATAGTCTGATCCCAGGTACAAGGCCCTTGTGAGCTGAGGC 1918
 1919 TGAAAGGCCTGTTTGGAGAGGCTGGGGTAGTGCCCAACCCAGCAGCCTTTCAGCAAATT 1978
 1979 GACTTTGGATGTGGACCCCTTCTCAGCCTGTACCAAGTACTGCAGTTGGCTAGGGATGCAG 2038
 2039 CTCAGTTTCCTGAGCATCCTTTGGAGCAGGTCAACCTGAGGCTCCTTTTGCTTACCCGAC 2098
 2099 ATCTAAGTTGTCCAGGTGCTCGGCTCCTGTGTGCCTGGATGACGGGAGGGCTCCGGGGTC 2158
 2159 TTTCAGTCAAAGACTTACATTGAGGTGGGGTGAGAGTCAGAGAAAAGTTCTGGTGCTTTT 2218
 2219 CATTTGTTCTAAGAGCTGAGAGCCAGGAATGCAGAGTCAATTGGGAAGGAGATGGGATAG 2278
 2279 CTGATGATCTTACCATGTCCATGACTGTGCCCCCTGATTCAAGACCGGATCATGTGGTGGC 2338
 2339 TTTATTTCTACACTTCTTGTCCACAATGGACAGTCTGAGGAAGCTCTTCTTTTCAGCCACA 2398
 2399 ACAACCACAGAAAGCCCTTCTTCTCCCCCTCTTGTCTCCATAAGTCAAAGCCATGTTT 2458
 2459 AGAACGGACCAGCCACCTTGCATGAAATCACTGAGTTCTGAAGCAACTTCAATTTCCA 2518
 2519 CGAGCCAAGTCCTGGGTCCAGGGACGCCCC 2548

Fig. 11

Rat	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu
	1				5					10					15	

Rat	Arg	Ile	Gln	Arg	Ala	Asn	Asp	Leu	Met	Gly	Leu	Asn	Glu
	*	*	*			*	*	*	*	*	*	*	
Bovine	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp

20
25

[illegible]

FO2250-14552660

Fig. 12

100 bp

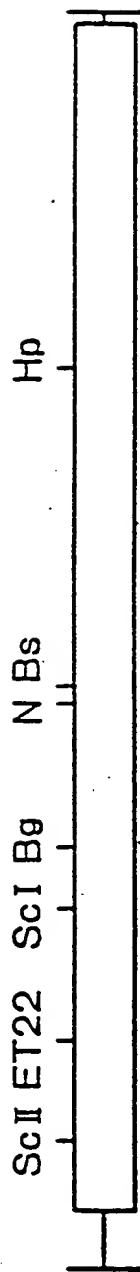


Fig. 13

1	AGCCCAGAGACACATTGGGGCTGACCTGCCGCTGCTGTCACTGGGAGGCCAGTGGTGGTGGCCAAGAAGTGTC																				ATG	78
1																					Met	1
77	GCT	GGT	GTC	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CAC	TGC	GGG	GCC	TGT	CCG	TGG	GGC	CGG	GGC		
2	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys	Pro	Trp	Gly	Arg	Gly		
																					136	
																					21	
137	AGA	CTC	CGC	AAA	GGA	CGC	GCA	GCC	TGC	AAG	TCC	GCG	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC		
22	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser	Ala	Ala	Gln	Arg	His	Ile	Gly	Ala	Asp		
																					196	
																					41	
197	CTG	CCG	CTG	CTG	TCA	GTG	GGA	GGC	CAG	TGG	TGC	TGG	CCA	AGA	AGT	GTC	ATG	GCT	GGT	GTC		
42	Leu	Pro	Leu	Leu	Ser	Val	Gly	Gly	Gln	Trp	Cys	Trp	Pro	Arg	Ser	Val	Met	Ala	Gly	Val		
																					256	
																					61	
257	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CTC	CTC	CTG	CTG	CCT	ATG	GCC	CCT	GCC	ATG	CAT	TCT	GAC		
62	Val	His	Val	Ser	Leu	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Met	Ala	Pro	Ala	Met	His	Ser	Asp		
																					316	
																					81	
317	TGC	ATC	TTC	AAG	AAG	GAG	CAA	GCC	ATG	TGC	CTG	GAG	AAG	ATC	CAG	AGG	GCC	AAT	GAG	CTG		
82	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu		
																					376	
																					101	
377	ATG	GGC	TTC	AAT	GAT	TCC	TCT	CCA	GGC	TGT	CCT	GGG	ATG	TGG	GAC	AAC	ATC	ACG	TGT	TGG		
102	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp		
																					436	
																					121	
437	AAG	CCC	GCC	CAT	GTG	GGT	GAG	ATG	GTC	CTG	GTC	AGC	TGC	CCT	GAG	CTC	TTC	CGA	ATC	TTC		
122	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	Leu	Phe	Arg	Ile	Phe		
																					496	
																					141	
497	AAC	CCA	GAC	CAA	GTC	TGG	GAG	ACC	GAA	ACC	ATT	GGA	GAG	TCT	GAT	TTT	GGT	GAC	AGT	AAC		
142	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe	Gly	Asp	Ser	Asn		
																					556	
																					161	
557	TCC	TTA	GAT	CTC	TCA	GAC	ATG	GGA	GTG	GTG	AGC	CGG	AAC	TGC	ACG	GAG	GAT	GGC	TGG	TCG		
162	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser		
																					616	
																					181	
617	GAA	CCC	TTC	CCT	CAT	TAC	TTT	GAT	GCC	TGT	GGG	TTT	GAT	GAA	TAT	GAA	TCT	GAG	ACT	GGG		
182	Glu	Pro	Phe	Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly		
																					676	
																					201	
677	GAC	CAG	GAT	TAT	TAC	TAC	CTG	TCA	GTG	AAG	GCC	CTC	TAC	ACG	GTT	GGC	TAC	AGC	ACA	TCC		
202	Asp	Gln	Asp	Tyr	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser		
																					736	
																					221	
737	CTC	GTC	ACC	CTC	ACC	ACT	GCC	ATG	GTC	ATC	CTT	TGT	CGC	TTC	CGG	AAG	CTG	CAC	TGC	ACA		
222	Leu	Val	Thr	Leu	Thr	Thr	Ala	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr		
																					796	
																					241	
737	CGC	AAC	TTC	ATC	CAC	ATG	AAC	CTG	TTT	GTG	TCG	TTC	ATG	CTG	AGG	GCG	ATC	TCC	GTC	TTC		
242	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe		
																					856	
																					261	
857	ATC	AAA	GAC	TGG	ATT	CTG	TAT	GCG	GAG	CAG	GAC	AGC	AAC	CAC	TGC	TTC	ATC	TCC	ACT	GTG		
262	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	His	Cys	Phe	Ile	Ser	Thr	Val		
																					916	
																					281	
917	GAA	TGT	AAG	GCC	GTC	ATG	GTT	TTC	TTC	CAC	TAC	TGT	GTT	GTG	TCC	AAC	TAC	TTC	TGG	CTG		
282	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	Tyr	Phe	Trp	Leu		
																					976	
																					301	
917	TTC	ATC	GAG	GGC	CTG	TAC	CTC	TTC	ACT	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCT	GAA	AGG	AGA		
302	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	Arg		
																					1036	
																					321	
1037	TAC	TTC	TAC	TGG	TAC	ACC	ATC	ATT	GGC	TGG	GGG	ACC	CCA	ACT	GTG	TGT	GTG	ACA	GTG	TGG		
322	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp		
																					1096	
																					341	
1097	GCT	ACG	CTG	AGA	CTC	TAC	TTT	GAT	GAC	ACA	GGC	TGC	TGG	GAT	ATG	AAT	GAC	AGC	ACA	GCT		
342	Ala	Thr	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala		
																					1156	
																					361	
1157	CTG	TGG	TGG	GTG	ATC	AAA	GGC	CCT	GTG	GTT	GGC	TCT	ATC	ATG	GTT	AAC	TTT	GTG	CTT	TTT		
362	Leu	Trp	Trp	Val	Ile	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe		
																					1216	
																					381	
1217	ATT	GGC	ATT	ATC	GTC	ATC	CTT	GTG	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAT	GAG		
382	Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu		
																					1276	
																					401	
1277	TCC	AGC	ATC	TAC	TTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG	CTG	CTC	ATC	CCA	CTA	TTC	GGA	ATC		
402	Ser	Ser	Ile	Tyr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile		
																					1336	
																					421	
1337	CAC	TAC	ACA	GTA	TTT	GCC	TTC	TCC	CCA	GAG	AAT	GTC	AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT		
422	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe		
																					1396	
																					441	
1397	GAG	CTG	GGG	CTG	GGC	TCC	TTC	CAG	GGC	TTT	GTG	GTG	GCT	GTT	CTC	TAC	TGT	TTT	CTG	AAT		
442	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn		
																					1456	
																					461	
1457	GGT	GAG	GTA	CAA	GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	GTG	AAC	CGT	TAC	TTC		
462	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	Asn	Arg	Tyr	Phe		
																					1516	
																					481	
1517	GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	GCC	AGC	AGT	GGG	GTG	AAT	GGG	GGC	ACC		
482	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	Thr		
																					1576	
																					501	
1577	CAG	CTC	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAA	ATC	CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC		
502	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp		
																					1636	
																					521	
1637	AAT	CTG	GCC	ACC	TGA	GCCATGCTCCCGT															1664	

Fig. 14

	20							25						
Human	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp
	*	*	*	*	*	*	*	*	*	*	*	*	*	*
Bovine	Glu	Lys	Ile	Gln	Arg	Val	Asn	Asp	Leu	Met	Gly	Leu	Asn	Asp

Rat		Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys
Type I-B	AAC	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG	
pHPR15A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys	
humanTypeI-B	AAT	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG	
pHPR55A	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	—	Cys	Val	Gln	Lys	Cys	Tyr	Cys	Lys	
Type I-B2	AAT	GAG	TCC	AGC	ATC	TAC	TTC	—	TGC	GTG	CAG	AAA	TGC	TAC	TGC	AAG	
pHPR66P	Asn	Glu	Ser	Ser	Ile	Tyr	Leu	Thr	Asn	Leu	Ser	Pro	Arg	Val	Pro	Lys	
Type I-C	AAT	GAG	TCC	AGC	ATC	TAC	TTA	ACA	AAT	TTA	AGC	CCG	CGA	GTC	CCC	AAG	

Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTA	TCC	ACC
Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC
Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr
CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC
Lys	Ala	Arg	Glu	Asp	Pro	Leu	Pro	Val	Pro	Ser	Asp	Gln	His	Ser	Leu
AAA	GCC	CGA	GAG	GAC	CCC	CTG	CCT	GTG	CCC	TCA	GAC	CAG	CAT	TCA	CTC

Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTA	CGG	CTG	GCC	CGC	TCC	ACC	CTA
		▲							
Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG
		▲							
Ile	Thr	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
ATT	ACT	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG
		▲							
Pro	Phe	Leu	Arg	Leu	Ala	Arg	Ser	Thr	Leu
CCT	TTC	CTG	CGA	CTG	GCC	CGG	TCC	ACC	CTG

1	A	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC	CTG	CCG	CTG	CTG	TCA	GTG	GGA	GGC	CAG	TGG	TGC	TGG	CCA	AGA	67
1	Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys	Pro	Trp	Gly	Arg	Gly			21
68	AGT	GTC	ATG	GCT	GGT	GTG	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CAC	TGC	GGG	GCC	TGT	CCG	TGG	GGC	CGG	GGC	136
22	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser	Ala	Ala	Gln	Arg	His	Ile	Gly	Ala	Asp	Leu	Pro	Leu	44
137	AGA	CTC	CGC	AAA	GGA	CGC	GCA	GCC	TGC	AAG	TCC	GCG	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC	CTG	CCG	CTG	205
45	Leu	Ser	Val	Gly	Gly	Gln	Trp	Cys	Trp	Pro	Arg	Ser	Val	Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	67
206	CTG	TCA	GTG	GGA	GGC	CAG	TGG	TGC	TGG	CCA	AGA	AGT	GTC	ATG	GCT	GGT	GTC	GTG	CAC	GTT	TCC	CTG	GCT	274
68	Ala	Leu	Leu	Leu	Leu	Pro	Met	Ala	Pro	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	90
275	GCT	CTC	CTC	CTG	CTG	CCT	ATG	GCC	CCT	GCC	ATG	CAT	TCT	GAC	TGC	ATC	TTC	AAG	AAG	GAG	CAA	GCC	ATG	343
91	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	113
344	TGC	CTG	GAG	AAG	ATC	CAG	AGG	GCC	AAT	GAG	CTG	ATG	GGC	TTC	AAT	GAT	TCC	TCT	CCA	GGC	TGT	CCT	GGG	412
114	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	136
413	ATG	TGG	GAC	AAC	ATC	ACG	TGT	TGG	AAG	CCC	GCC	CAT	GTG	GGT	GAG	ATG	GTC	CTG	GTC	ACC	TGC	CCT	GAG	481
137	Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe	Gly	Asp	159
482	CTC	TTC	CGA	ATC	TTC	AAC	CCA	GAC	CAA	GTC	TGG	GAG	ACC	GAA	ACC	ATT	GGA	GAG	TCT	GAT	TTT	GGT	GAC	550
160	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	182
551	AGT	AAC	TCC	TTA	GAT	CTC	TCA	GAC	ATG	GGA	GTG	GTG	AGC	CGG	AAC	TCC	ACG	GAG	GAT	GGC	TGG	TCC	GAA	619
183	Pro	Phe	Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	205
620	CCC	TTC	CCT	CAT	TAC	TTT	GAT	GCC	TGT	GGG	TTT	GAT	GAA	TAT	GAA	TCT	GAG	ACT	GGG	GAC	CAG	GAT	TAT	688
206	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	228
689	TAC	TAC	CTG	TCA	GTG	AAG	GCC	CTC	TAC	ACG	GTT	GGC	TAC	AGC	ACA	TCC	CTC	GTC	ACC	CTC	ACC	ACT	GCC	757
229	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	251
758	ATG	GTC	ATC	GTT	TGT	CGC	TTC	CGG	AAG	CTG	CAC	TGC	ACA	CGC	AAC	TTC	ATC	CAC	ATG	AAC	CTG	TTT	GTG	826
252	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	274
827	TCG	TTC	ATG	CTG	AGG	GCG	ATC	TCC	GTC	TTC	ATC	AAA	GAC	TGG	ATT	CTG	TAT	GCG	GAG	CAG	GAC	AGC	AAC	895
279	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	297
896	CAC	TGC	TTC	ATC	TCC	ACT	GTG	GAA	TGT	AAG	GCC	GTG	ATG	GTT	TTC	TTC	CAC	TAC	TGT	GTT	GTG	TCC	AAC	964
298	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	320
965	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAC	CTC	TTC	ACT	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCT	GAA	AGG	1033
321	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	343
1034	AGA	TAC	TTC	TAC	TGG	TAC	ACC	ATC	ATT	GGC	TGG	GGG	ACC	CCA	ACT	GTG	TGT	GTG	ACA	GTG	TGG	GCT	ACG	1102
344	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val	Ile	366
1103	CTG	AGA	CTC	TAC	TTT	GAT	GAC	ACA	GGC	TGC	TGG	GAT	ATG	AAT	GAC	AGC	ACA	GCT	CTG	TGG	TGG	GTG	ATC	1171
367	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	389
1172	AAA	GGC	CCT	GTG	GTT	GGC	TCT	ATC	ATG	GTT	AAC	TTT	GTG	CTT	TTT	ATT	GGC	ATT	ATC	GTC	ATC	CTT	GTG	1240
390	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Ser	Cys	Val	Gln	Lys	Cys	412
1241	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAT	GAG	TCC	AGC	ATC	TAC	TTC	AGC	TGC	GTG	CAG	AAA	TGC	1309
413	Tyr	Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	435
1310	TAC	TGC	AAG	CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC	ATT	ACT	CTG	CGA	1378
436	Leu	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	458
1379	CTG	GCC	CGG	TCC	ACC	CTG	CTG	CTC	ATC	CCA	CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	TCC	CCA	1447
459	Glu	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	481
1448	GAG	AAT	GTC	AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	CTG	GGC	TCC	TTC	CAG	GGC	TTT	GTG	GTG	1516
482	Ala	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	504
1517	GCT	GTT	CTC	TAC	TGT	TTT	CTG	AAT	GGT	GAG	GTA	CAA	GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	1585
505	Val	Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	527
1586	GTG	AAC	CGT	TAC	TTC	GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	GCC	AGC	AGT	GGG	GTG	AAT	GGG	1654
528	Gly	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	550
1655	GGC	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAA	ATC	CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	1723
551	Leu	Ala	Thr	***																				553
1724	CTG	GCC	ACC	TGA	GCC	ATG	CTC	CCC	T															1748

Fig. 17

1	A	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC	CTG	CGG	CTG	CTG	TCA	GTG	GGA	GCC	CAG	TGG	TGC	TGG	CCA	AGA	67
1			Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	Ala	His	Cys	Gly	Ala	Cys	Pro	Trp	Gly	Arg	Gly	21
68	AGT	GTC	ATG	GCT	GGT	GTC	GTG	CAC	GTT	TCC	CTG	GCT	GCT	CAC	TGC	GGG	GCC	TGT	CCG	TGG	GGC	CGG	GGC	136
22	Arg	Leu	Arg	Lys	Gly	Arg	Ala	Ala	Cys	Lys	Ser	Ala	Ala	Gln	Arg	His	Ile	Gly	Ala	Asp	Leu	Pro	Leu	44
137	AGA	CTC	CGC	AAA	GGA	CGC	GCA	GCC	TGC	AAG	TCC	CGC	GCC	CAG	AGA	CAC	ATT	GGG	GCT	GAC	CTG	CCG	CTG	205
48	Leu	Ser	Val	Gly	Gly	Gln	Trp	Cys	Trp	Pro	Arg	Ser	Val	Met	Ala	Gly	Val	Val	His	Val	Ser	Leu	Ala	67
206	CTG	TCA	GTG	GGA	GGC	CAG	TGG	TGC	TGG	CCA	AGA	AGT	GTC	ATG	GCT	GGT	GTC	GTG	CAC	GTT	TCC	CTG	GCT	274
68	Ala	Leu	Leu	Leu	Leu	Pro	Met	Ala	Pro	Ala	Met	His	Ser	Asp	Cys	Ile	Phe	Lys	Lys	Glu	Gln	Ala	Met	90
275	GCT	CTC	CTC	CTG	CTG	CCT	ATG	GCC	CCT	GCC	ATG	CAT	TCT	GAC	TGC	ATC	TTC	AAG	AAG	GAG	CAA	GCC	ATG	343
91	Cys	Leu	Glu	Lys	Ile	Gln	Arg	Ala	Asn	Glu	Leu	Met	Gly	Phe	Asn	Asp	Ser	Ser	Pro	Gly	Cys	Pro	Gly	113
344	TGC	CTG	GAG	AAG	ATC	CAG	AGG	GCC	AAT	GAG	CTG	ATG	GGC	TTC	AAT	GAT	TCC	TCT	CCA	GGC	TGT	CCT	GGG	412
114	Met	Trp	Asp	Asn	Ile	Thr	Cys	Trp	Lys	Pro	Ala	His	Val	Gly	Glu	Met	Val	Leu	Val	Ser	Cys	Pro	Glu	136
413	ATG	TGG	GAC	AAC	ATC	ACG	TGT	TGG	AAG	CCC	GCC	CAT	GTG	GGT	GAG	ATG	GTC	CTG	GTC	ACC	TGC	CCT	GAG	481
137	Leu	Phe	Arg	Ile	Phe	Asn	Pro	Asp	Gln	Val	Trp	Glu	Thr	Glu	Thr	Ile	Gly	Glu	Ser	Asp	Phe	Gly	Asp	159
482	CTC	TTC	CGA	ATC	TTC	AAC	CCA	GAC	CAA	GTC	TGG	GAG	ACC	GAA	ACC	ATT	GGA	GAG	TCT	GAT	TTT	GGT	GAC	550
160	Ser	Asn	Ser	Leu	Asp	Leu	Ser	Asp	Met	Gly	Val	Val	Ser	Arg	Asn	Cys	Thr	Glu	Asp	Gly	Trp	Ser	Glu	182
551	AGT	AAC	TCC	TTA	GAT	CTC	TCA	GAC	ATG	GGA	GTG	GTG	AGC	CGG	AAC	TGC	ACG	GAG	GAT	GGC	TGG	TCG	GAA	619
183	Pro	Phe	Pro	His	Tyr	Phe	Asp	Ala	Cys	Gly	Phe	Asp	Glu	Tyr	Glu	Ser	Glu	Thr	Gly	Asp	Gln	Asp	Tyr	205
620	CCC	TTC	CCT	CAT	TAC	TTT	GAT	GCC	TGT	GGG	TTT	GAT	GAA	TAT	GAA	TCT	GAG	ACT	GGG	GAC	CAG	GAT	TAT	688
206	Tyr	Tyr	Leu	Ser	Val	Lys	Ala	Leu	Tyr	Thr	Val	Gly	Tyr	Ser	Thr	Ser	Leu	Val	Thr	Leu	Thr	Thr	Ala	228
689	TAC	TAC	CTG	TCA	GTG	AAG	GCC	CTC	TAC	ACG	GTT	GGC	TAC	AGC	ACA	TCC	CTC	GTG	ACC	CTC	ACC	ACT	GCC	757
229	Met	Val	Ile	Leu	Cys	Arg	Phe	Arg	Lys	Leu	His	Cys	Thr	Arg	Asn	Phe	Ile	His	Met	Asn	Leu	Phe	Val	251
758	ATG	GTC	ATC	CTT	TGT	CGC	TTC	CGG	AAG	CTG	CAC	TGC	ACA	CGC	AAC	TTC	ATC	CAC	ATG	AAC	CTG	TTT	GTG	826
252	Ser	Phe	Met	Leu	Arg	Ala	Ile	Ser	Val	Phe	Ile	Lys	Asp	Trp	Ile	Leu	Tyr	Ala	Glu	Gln	Asp	Ser	Asn	274
827	TCG	TTC	ATG	CTG	AGG	GCG	ATC	TCC	GTC	TTC	ATC	AAA	GAC	TGG	ATT	CTG	TAT	GCG	GAG	CAG	GAC	AGC	AAC	895
275	His	Cys	Phe	Ile	Ser	Thr	Val	Glu	Cys	Lys	Ala	Val	Met	Val	Phe	Phe	His	Tyr	Cys	Val	Val	Ser	Asn	297
896	CAC	TGC	TTC	ATC	TCC	ACT	GTG	GAA	TGT	AAG	GCC	GTC	ATG	GTT	TTC	TTC	CAC	TAC	TGT	GTT	GTG	TCC	AAC	964
298	Tyr	Phe	Trp	Leu	Phe	Ile	Glu	Gly	Leu	Tyr	Leu	Phe	Thr	Leu	Leu	Val	Glu	Thr	Phe	Phe	Pro	Glu	Arg	320
965	TAC	TTC	TGG	CTG	TTC	ATC	GAG	GGC	CTG	TAC	CTC	TTC	ACT	CTG	CTG	GTG	GAG	ACC	TTC	TTC	CCT	GAA	AGG	1033
321	Arg	Tyr	Phe	Tyr	Trp	Tyr	Thr	Ile	Ile	Gly	Trp	Gly	Thr	Pro	Thr	Val	Cys	Val	Thr	Val	Trp	Ala	Thr	343
1034	AGA	TAC	TTC	TAC	TGG	TAC	ACC	ATC	ATT	GGC	TGG	GGG	ACC	CCA	ACT	GTG	TGT	GTG	ACA	GTG	TGG	GCT	ACG	1102
344	Leu	Arg	Leu	Tyr	Phe	Asp	Asp	Thr	Gly	Cys	Trp	Asp	Met	Asn	Asp	Ser	Thr	Ala	Leu	Trp	Trp	Val	Ile	366
103	CTG	AGA	CTC	TAC	TTT	GAT	GAC	ACA	GGC	TGC	TGG	GAT	ATG	AAT	GAC	AGC	ACA	GCT	CTG	TGG	TGG	GTG	ATC	1171
367	Lys	Gly	Pro	Val	Val	Gly	Ser	Ile	Met	Val	Asn	Phe	Val	Leu	Phe	Ile	Gly	Ile	Ile	Val	Ile	Leu	Val	389
172	AAA	GGC	CCT	GTG	GTT	GGC	TCT	ATC	ATG	GTT	AAC	TTT	GTG	CTT	TTT	ATT	GGC	ATT	ATC	GTC	ATC	CTT	GTG	1240
390	Gln	Lys	Leu	Gln	Ser	Pro	Asp	Met	Gly	Gly	Asn	Glu	Ser	Ser	Ile	Tyr	Phe	Cys	Val	Gln	Lys	Cys	Tyr	412
241	CAG	AAA	CTT	CAG	TCT	CCA	GAC	ATG	GGA	GGC	AAT	GAG	TCC	AGC	ATC	TAC	TTC	TGC	GTG	CAG	AAA	TGC	TAC	1309
413	Cys	Lys	Pro	Gln	Arg	Ala	Gln	Gln	His	Ser	Cys	Lys	Met	Ser	Glu	Leu	Ser	Thr	Ile	Thr	Leu	Arg	Leu	435
310	TGC	AAG	CCA	CAG	CGG	GCT	CAG	CAG	CAC	TCT	TGC	AAG	ATG	TCA	GAA	CTG	TCC	ACC	ATT	ACT	CTG	CGA	CTG	1378
436	Ala	Arg	Ser	Thr	Leu	Leu	Leu	Ile	Pro	Leu	Phe	Gly	Ile	His	Tyr	Thr	Val	Phe	Ala	Phe	Ser	Pro	Glu	458
379	GCC	CGG	TCC	ACC	CTG	CTG	CTC	ATC	CCA	CTA	TTC	GGA	ATC	CAC	TAC	ACA	GTA	TTT	GCC	TTC	TCC	CCA	GAG	1447
459	Asn	Val	Ser	Lys	Arg	Glu	Arg	Leu	Val	Phe	Glu	Leu	Gly	Leu	Gly	Ser	Phe	Gln	Gly	Phe	Val	Val	Ala	481
1448	AAT	GTC	AGC	AAA	AGG	GAA	AGA	CTC	GTG	TTT	GAG	CTG	GGG	CTG	GGC	TCC	TTC	CAG	GGC	TTT	GTG	GTG	GCT	1516
482	Val	Leu	Tyr	Cys	Phe	Leu	Asn	Gly	Glu	Val	Gln	Ala	Glu	Ile	Lys	Arg	Lys	Trp	Arg	Ser	Trp	Lys	Val	504
1517	GTT	CTC	TAC	TGT	TTT	CTG	AAT	GGT	GAG	GTA	CAA	GCG	GAG	ATC	AAG	CGA	AAA	TGG	CGA	AGC	TGG	AAG	GTG	1585
505	Asn	Arg	Tyr	Phe	Ala	Val	Asp	Phe	Lys	His	Arg	His	Pro	Ser	Leu	Ala	Ser	Ser	Gly	Val	Asn	Gly	Gly	527
1586	AAC	CGT	TAC	TTC	GCT	GTG	GAC	TTC	AAG	CAC	CGA	CAC	CCG	TCT	CTG	GCC	AGC	AGT	GGG	GTG	AAT	GGG	GGC	1654
528	Thr	Gln	Leu	Ser	Ile	Leu	Ser	Lys	Ser	Ser	Ser	Gln	Ile	Arg	Met	Ser	Gly	Leu	Pro	Ala	Asp	Asn	Leu	550
1655	ACC	CAG	CTC	TCC	ATC	CTG	AGC	AAG	AGC	AGC	TCC	CAA	ATC	CGC	ATG	TCT	GGC	CTC	CCT	GCT	GAC	AAT	CTG	1723
551	Ala	Thr	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	552
724	GCC	ACC	TGA	GCC	ATG	CTC	CCC	T	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1745

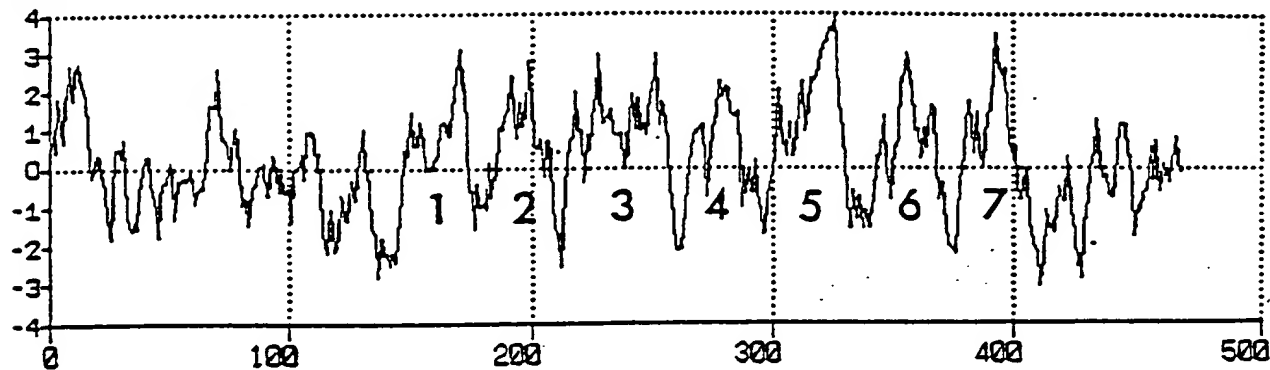
Fig. 18

[illegible]

Fig. 19

A

Index



B

Index

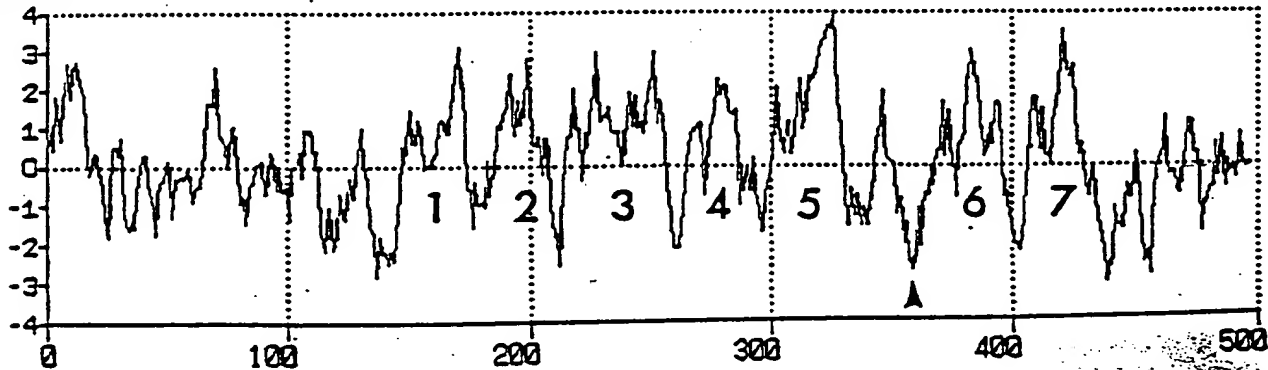


Fig. 20

EQUIVALENT

- 1 : Ala(A), Ser(S), Thr(T), Pro(P), Gly(G)
- 2 : Asn(N), Asp(D), Asx(B), Glu(E), Gln(Q), Glx(Z)
- 3 : His(H), Arg(R), Lys(K)
- 4 : Met(M), Leu(L), Ile(I), Val(V)
- 5 : Phe(F), Tyr(Y), Trp(W)

PACAP receptor (upper lines)

VIP receptor (lower lines)

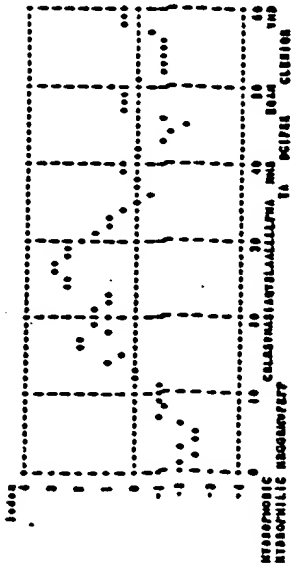
19	29	39	49	59	69	79
TALLLPVAIAMHSDC	IFKKEQAMCLER	IQRANDLMGLN	ESSPGCPGMWDN	ITCWKPAQVGEM	VLVSCPEV	
* *	**	* *	*	* *	* *	**
MRPPSPPHVRWLCV	LAGALACALRP	AGSQAASPOHE	CEYLQLIEIQ	RQQCLEEAQLE	NETTGCSKMWDN	L
10	20	30	40	50	60	70
89	99	109	119	129	139	149
FRIFNPDQVWMTET	IGDSGFADSNS	LEITDMGVVGR	NCTEDGWSEPF	PHYFDACGFDD	YEPESGDQDY	YYY
*	*	**	***	* *	* *	*
TCWPTTPRGQAVV	LDCLIFQLFAP	IHGYNISRSCT	EEGWSQLEPG	PHYIACGLNDR	ASSLDEQQQT	KFY
80	90	100	110	120	130	140
159	169	179	189	199	209	219
LSVKALYTVGYST	SLATLTAMVIL	CRFRKLHCTR	NFIHMNLFV	SFMLRAISV	FIKDWILYAE	QDSSHCF
****	*****	*****	** *	*****	*****	*****
NTVKTGYTIGYSL	SLASLLVAMAIL	SLFRKLHCTR	NYIHMHLFMS	FILRATAVFI	KDMALFNSGE	IDHCS
150	160	170	180	190	200	210
229	239	249	259	269	279	289
VSTVECKAVMVFF	HYCVVSNYFW	LFIGLYLFTLL	VETFFPERRY	FYWYTIIGW	GTPVCVTVW	AVLRLY
***	***	***	*****	*****	*	*****
EASVGCKAAVVFF	QYCVMANFFW	LLVEGLYLYT	LLAVSFFSER	KYFWGYILIG	WGVPSVFI	TITVTVRIY
220	230	240	250	260	270	280
299	309	319	329	339	349	359
FDDAGCWDMDN	STALWWVIKGP	VGSIMVNFV	LFIGIIILVQ	KLQSPDMG	GNESSIYLRL	ARSTLLIP
***	****	*****	*****	**	*****	*****
FEDFGCWDTI	INSSLWIIKAP	ILLSILVNFV	LFIGIIRILV	QKLRRPPDI	GKNDSSPYS	RSLAKSTLLIP
290	300	310	320	330	340	350
369	379	389	399	409	419	429
LFGIHYTVFAF	SPENVSKRER	LVFELGLGS	FQGFVVAVLY	CFLNGEVQAE	IKRKWRSWK	VNRYFTMDFKH
*****	****	***	*****	*****	*****	*****
LFGIHYVMFAFF	PDNFKAQVKM	VFELVVG	SFQGFVVAIL	YCFLNGEVQAE	LRKWRRLQ	GVLGWSSKS
360	370	380	390	400	410	420
439	449	459				
RHPSLASSGVNG	TQLSILSKSS	SQLRMSSL	PADNLAT*			
**	** *	*****	**	* *	***	
QHPWGGSN	GATCSTQV	SMLTRVSP	SARRSSSF	QAEVSLV		
430	440	450				

HUMAN
BOVINE
RAT

70255 70255 70255

Fig. 23

*** HYDROPHOBICITY INDEX ***
 WINDOW 0 MEAN INDEX 0.00 (7000 1 TO 910)
 THRESHOLD LINE 0.00



DATE 11-10-10

ANALYSIS LIST *****

*** INPUT INFORMATION ***

FILE NAME : 214-10-10

HYPERMORPHIC INDEX TABLE FILE : DATA.DAT

*** HYPERMORPHIC INDEX ***

WINDOW : 5 MEAN INDEX : 0.10 (FROM 1 TO 10)

THRESHOLD LINE : 0.00

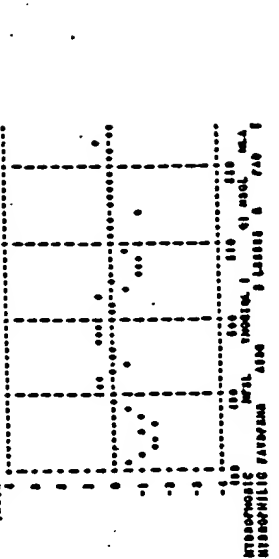
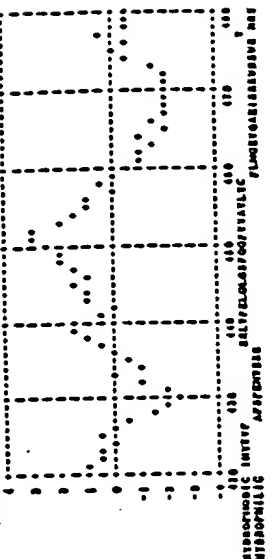
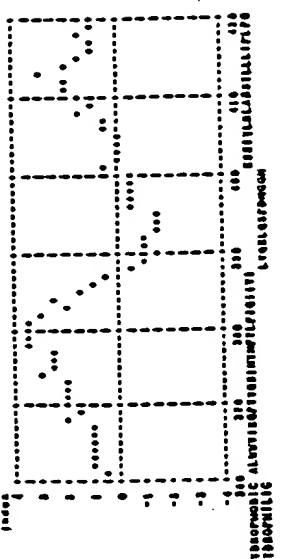
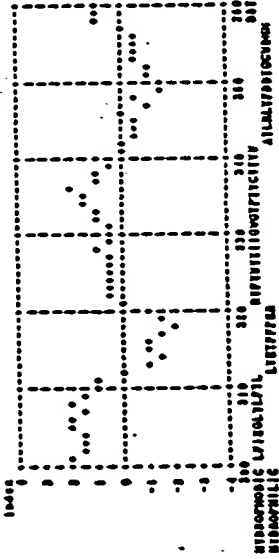
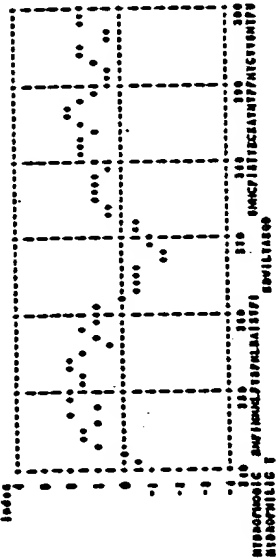
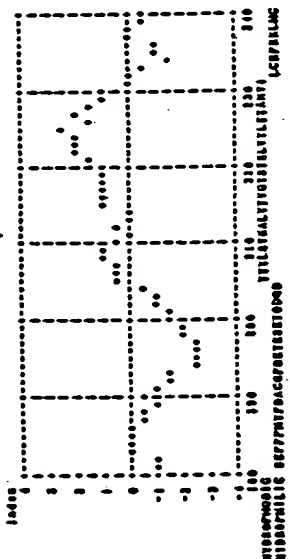
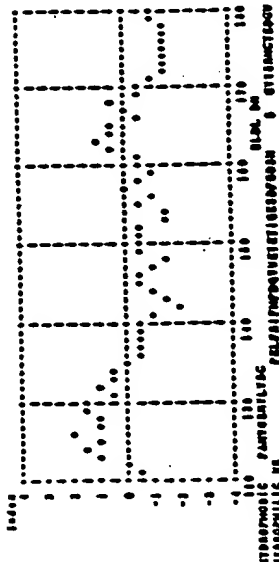
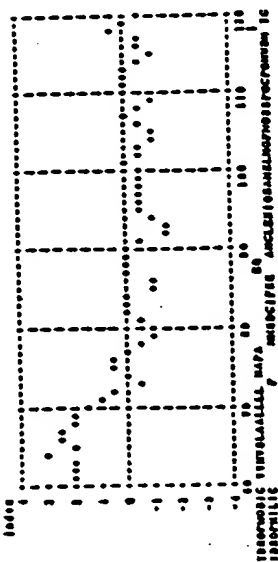
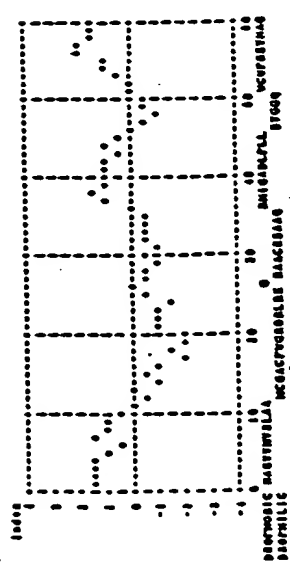


Fig. 28

ABSORBANCE AT 214 NM

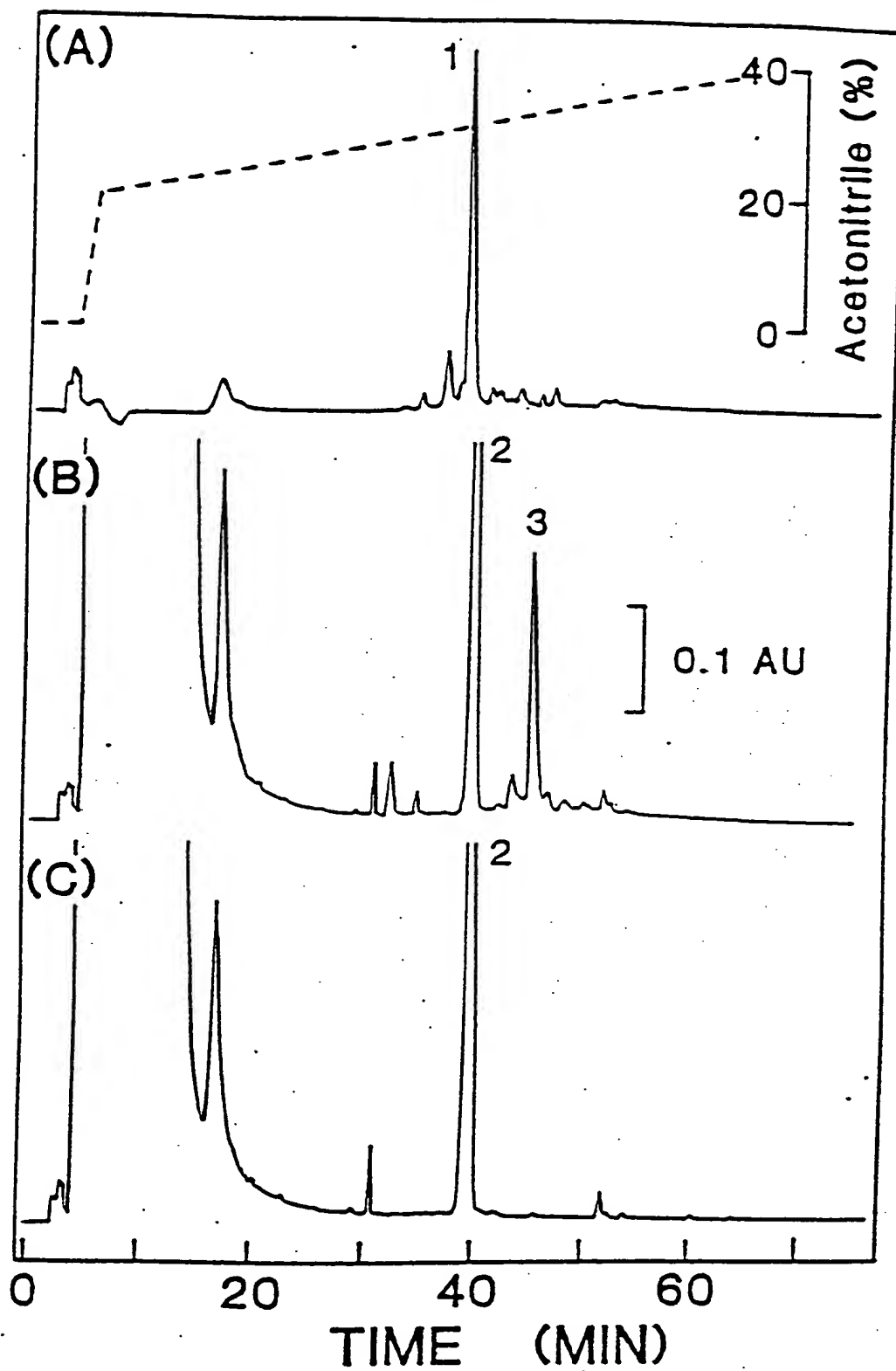


Fig. 29

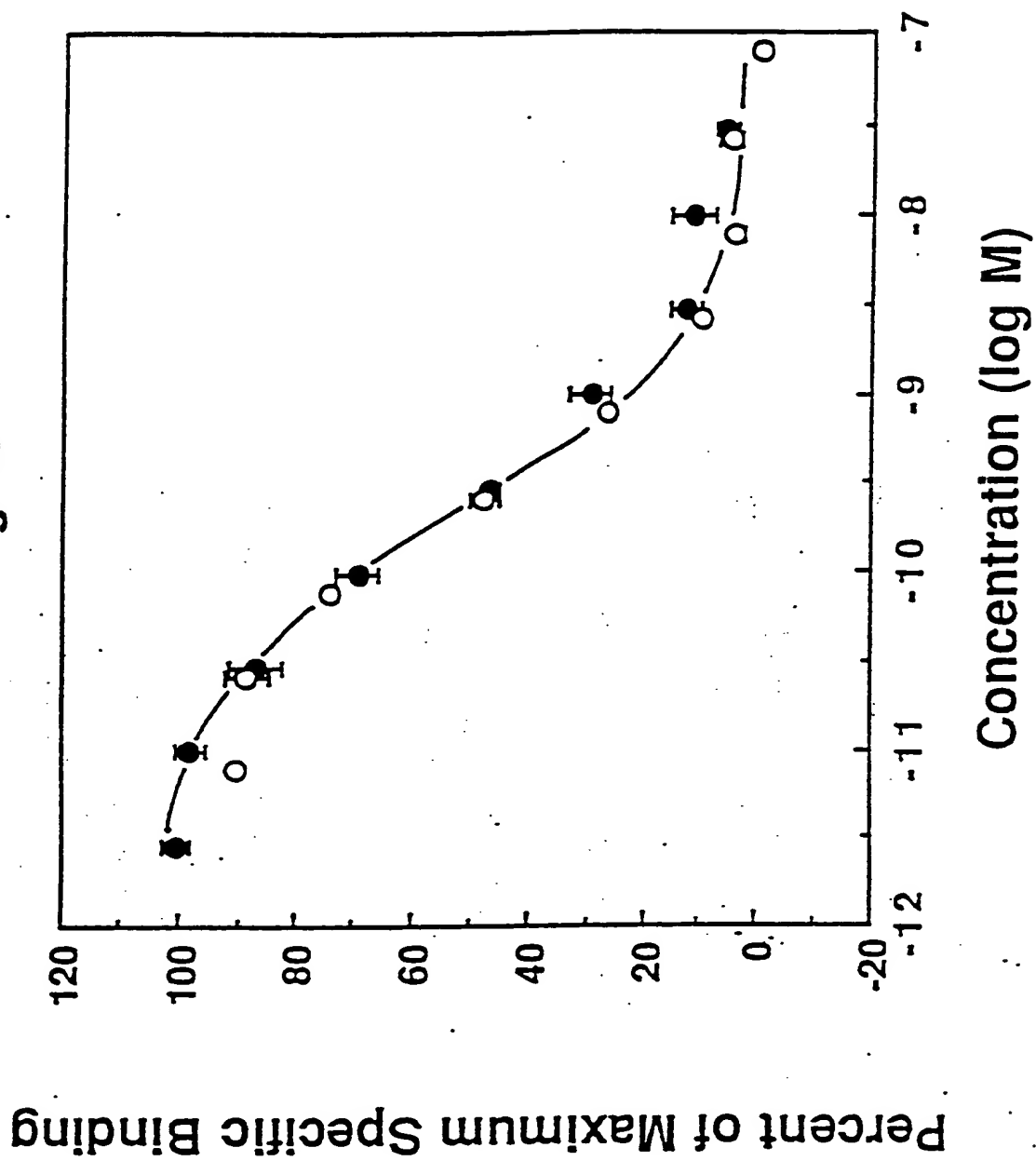


Fig. 30

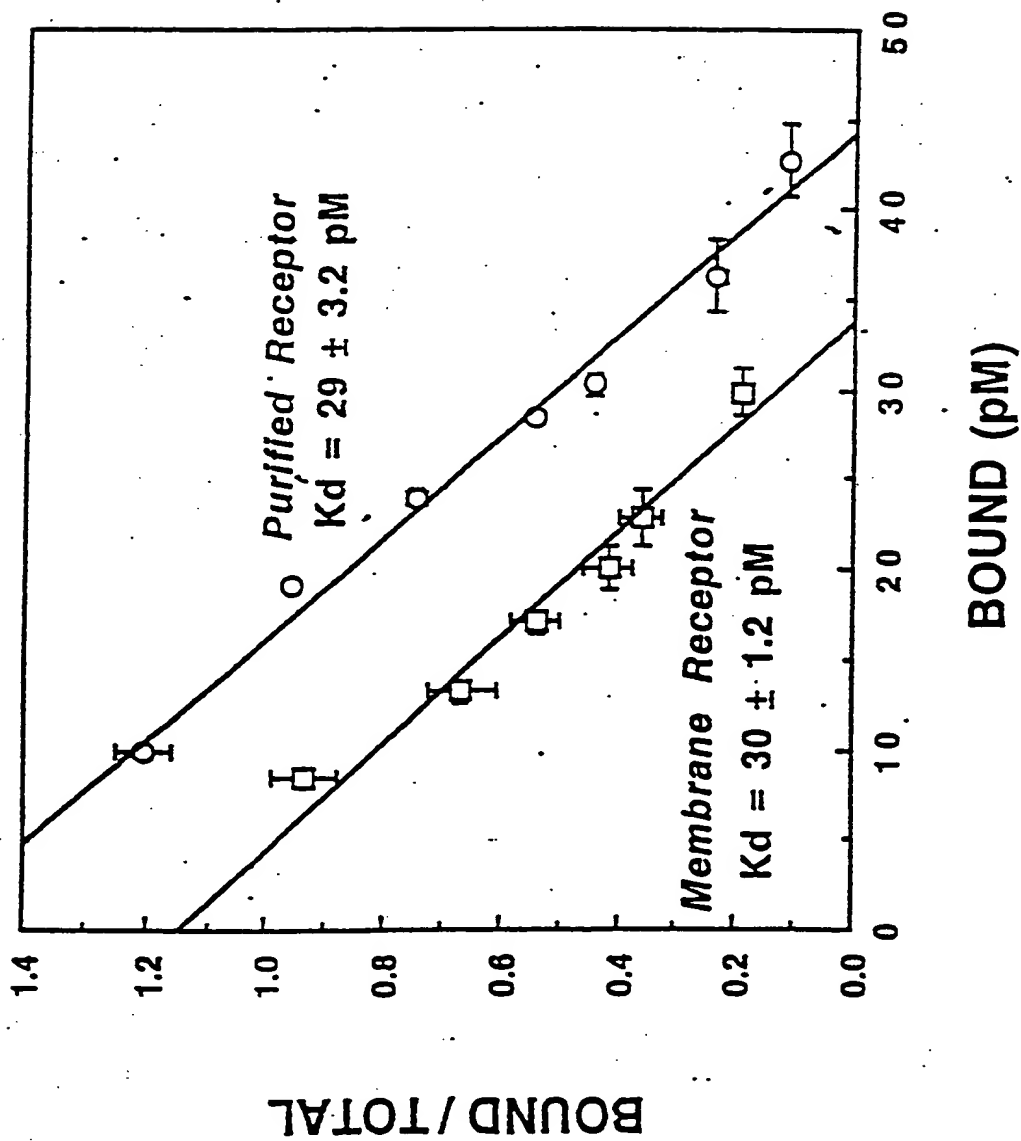
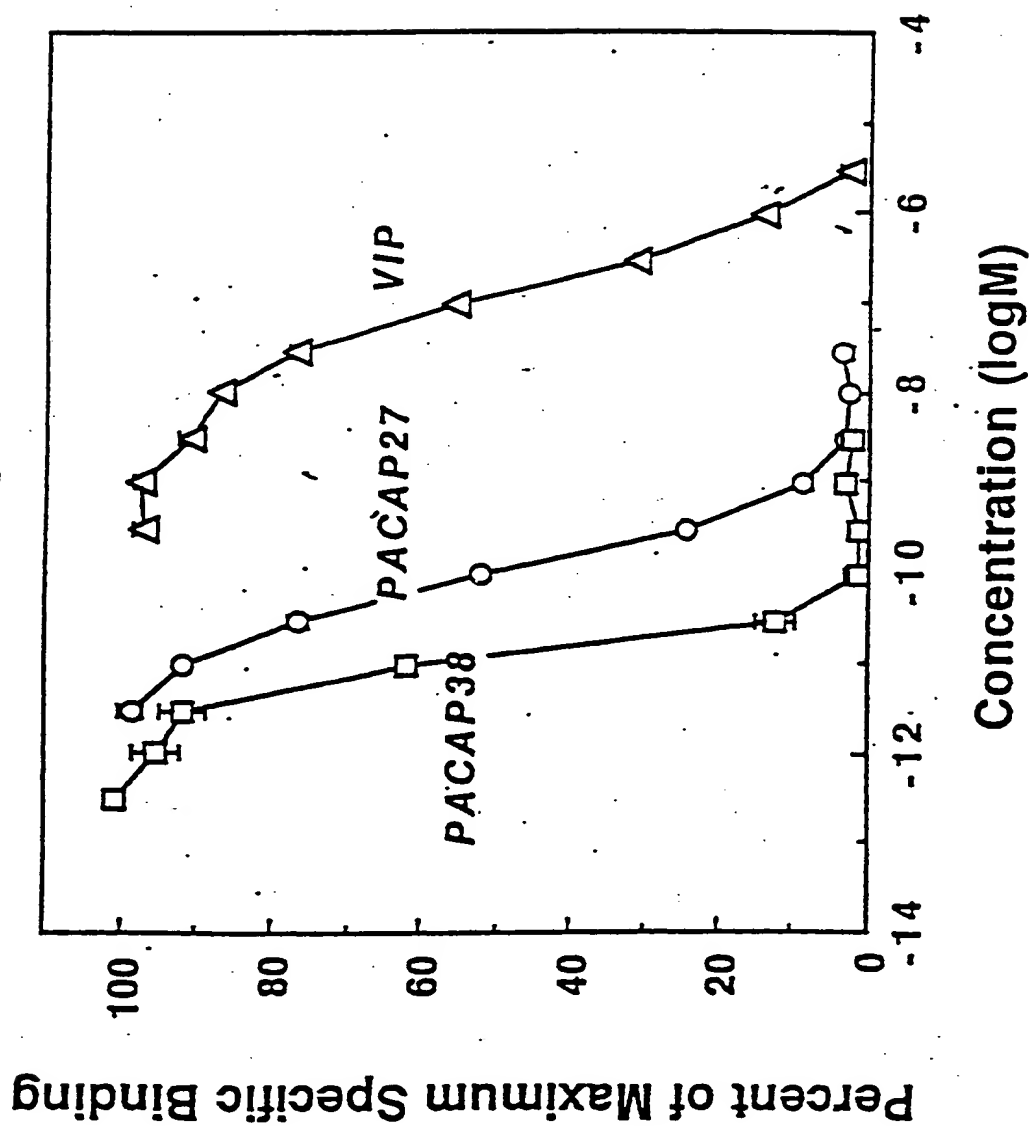


Fig. 31



A high-contrast, black and white photograph of a textured surface, possibly a book cover or endpaper. The image is characterized by a dense, grainy texture. A vertical strip of dark material runs down the left side. In the center-right, there is a small, dark, irregular shape that resembles a hole or a mark. The overall appearance is that of a heavily worn or damaged surface.

[illegible]

Fig. 33

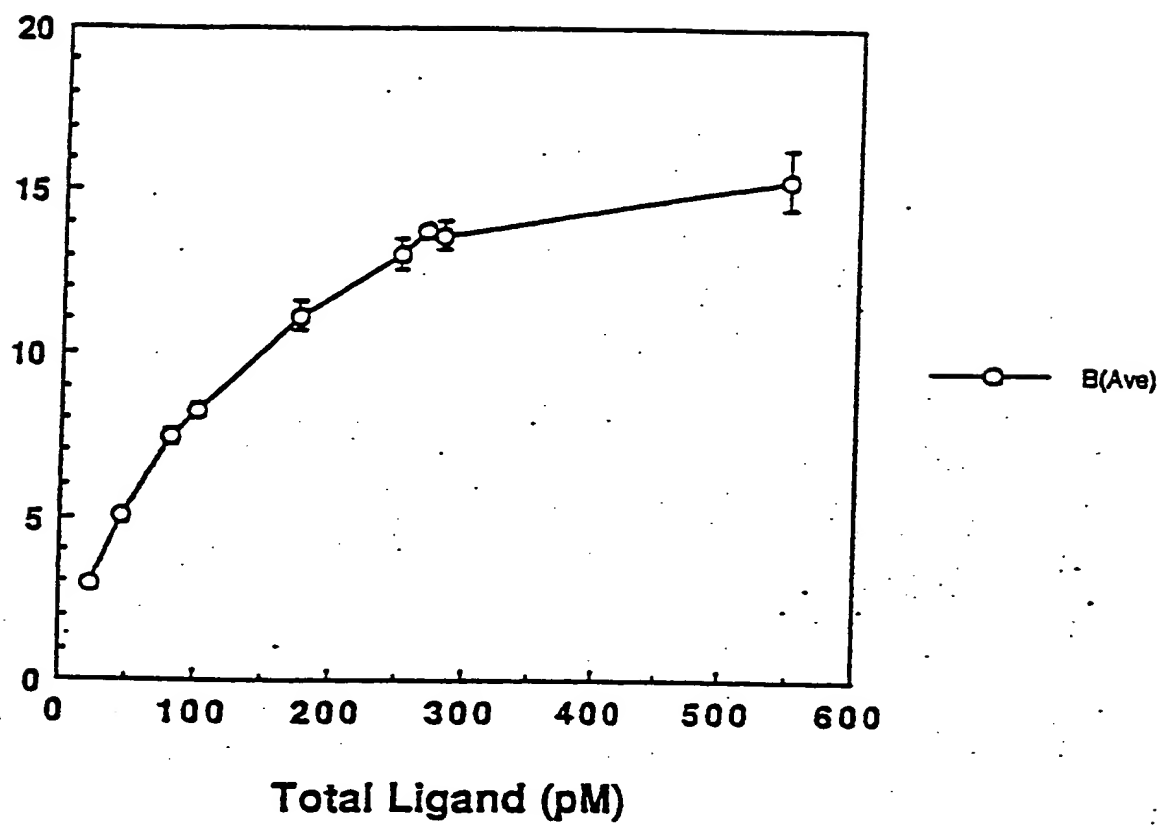


Fig. 34

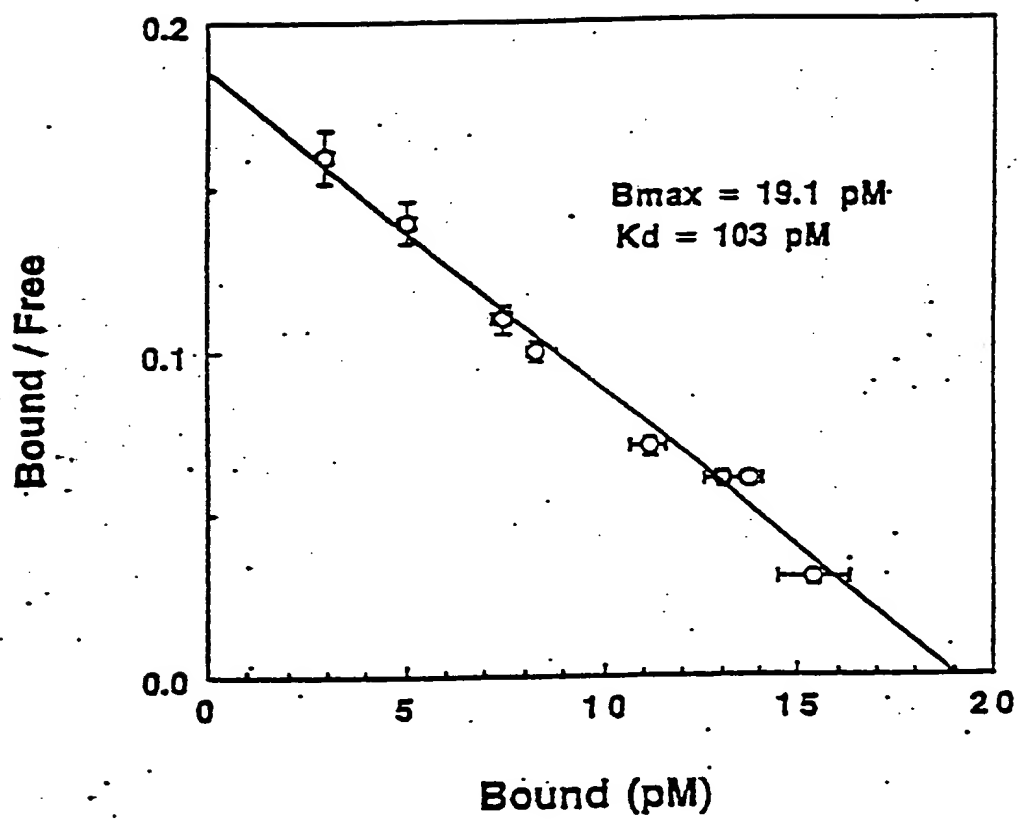


Fig. 35

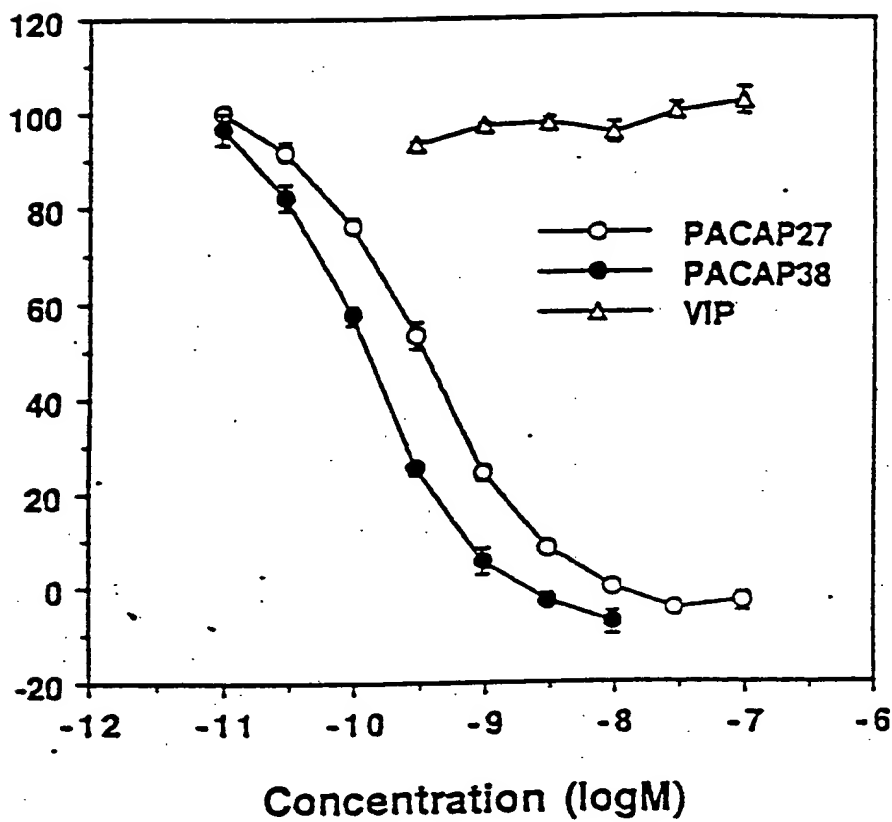


Fig. 36

Increase of Intracellular cAMP Concentration
(-fold of control)

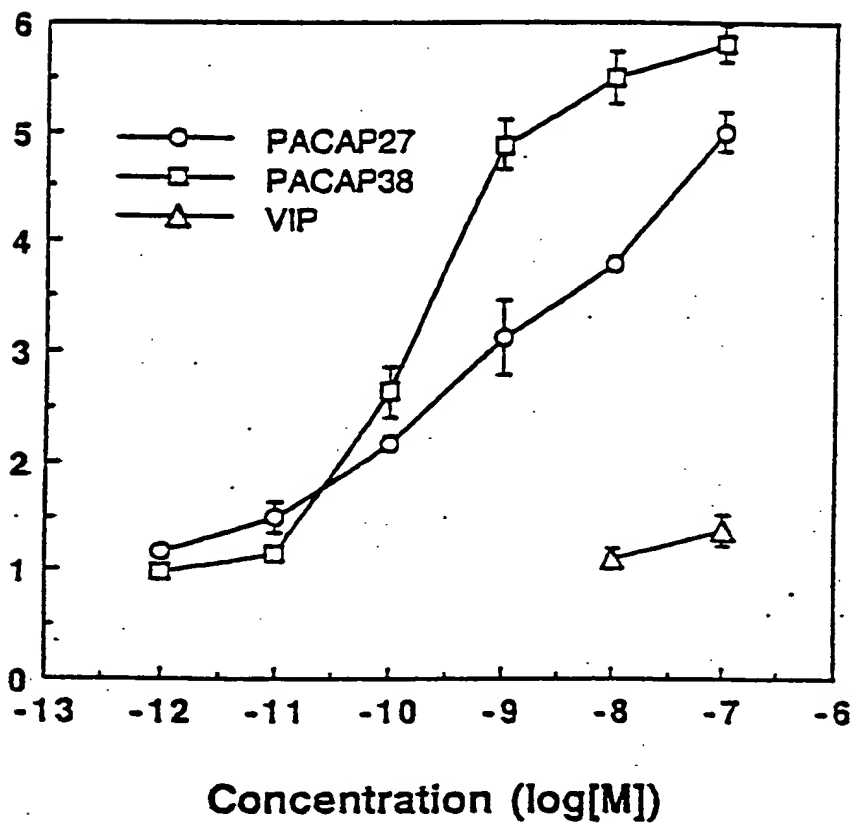


Fig. 37

Accumulation of Inositolphosphates
(-fold of control)

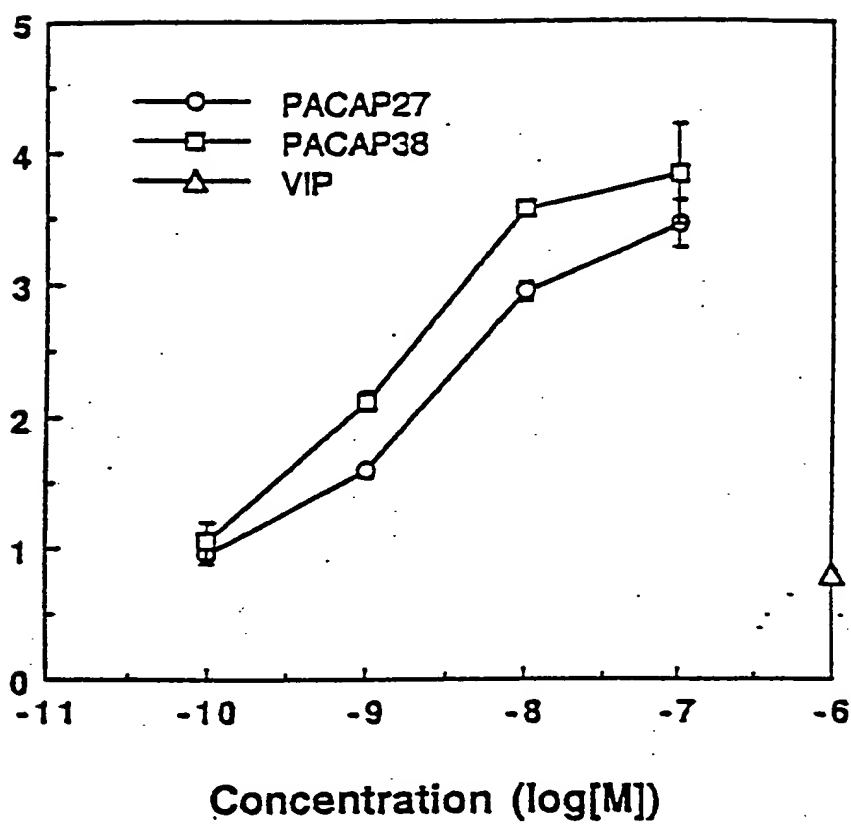


Fig. 38

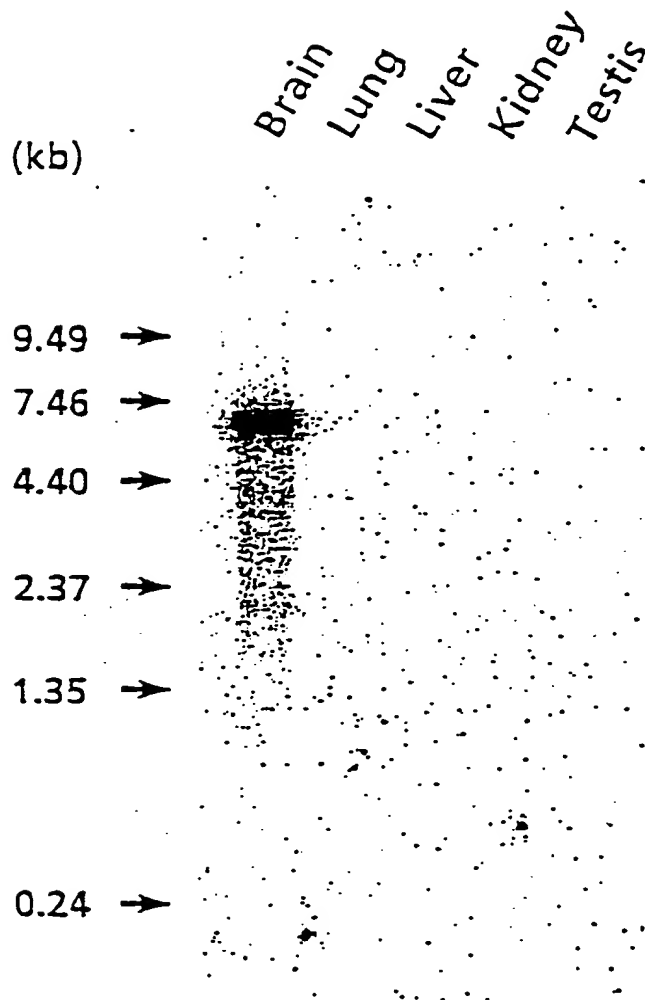


Fig. 39

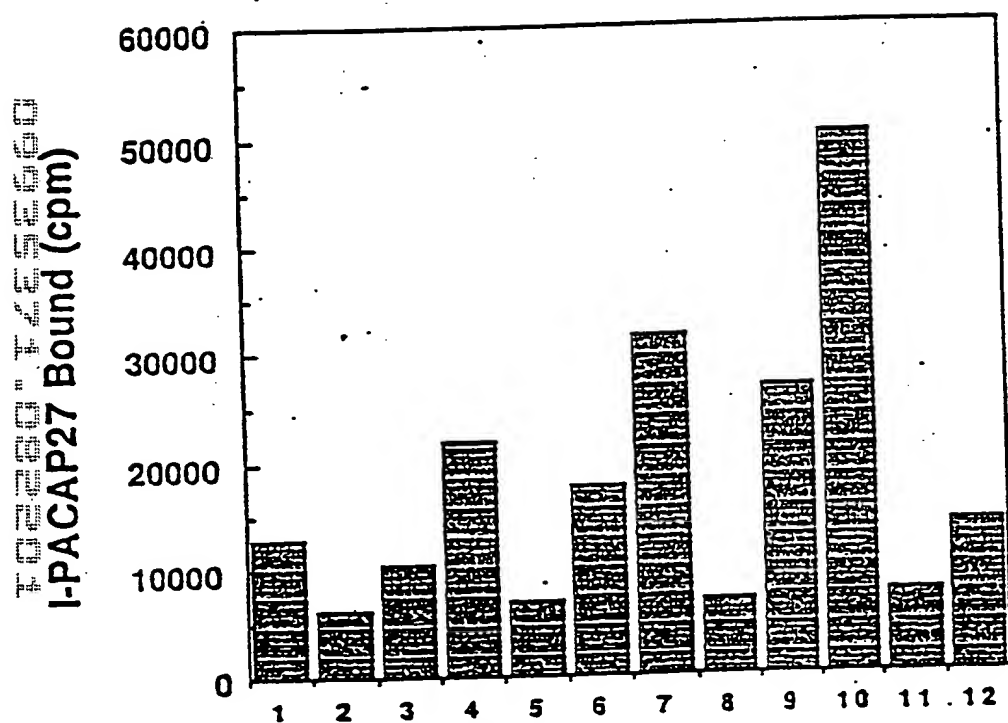
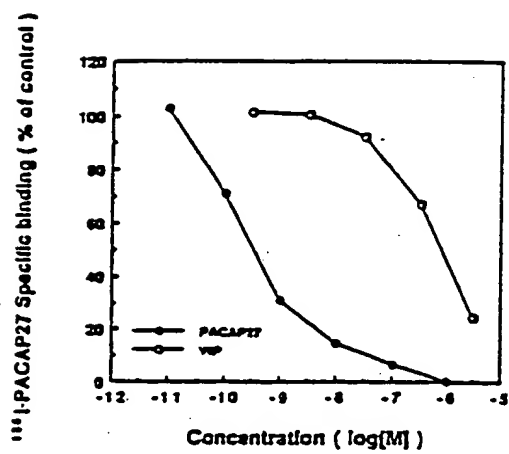


Fig. 40

A



B

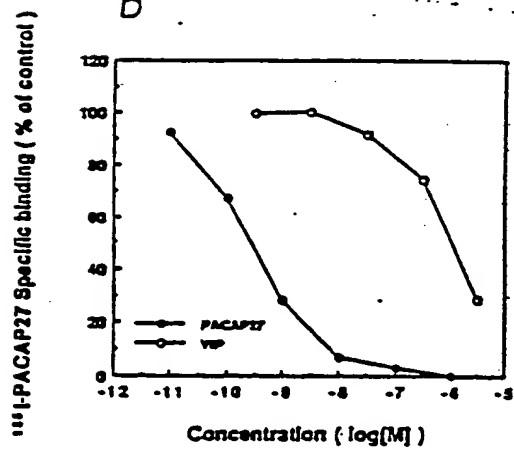


Fig. 41

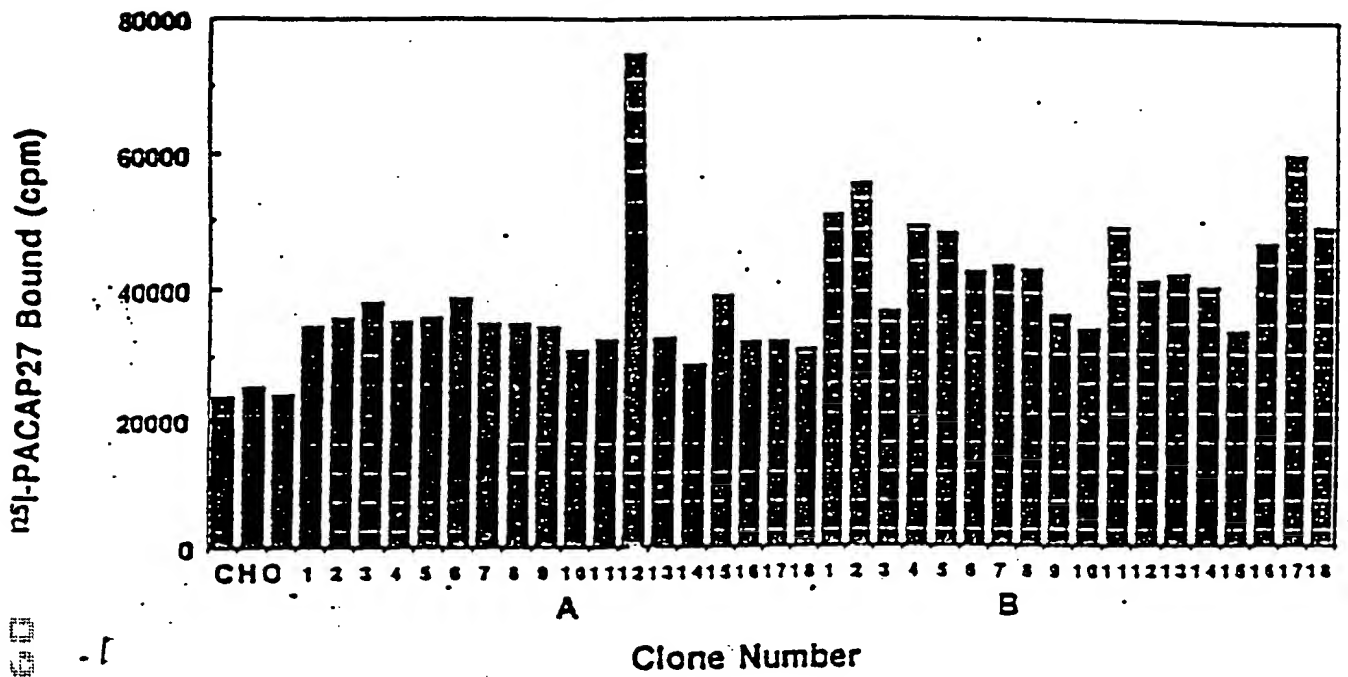


Fig. 42

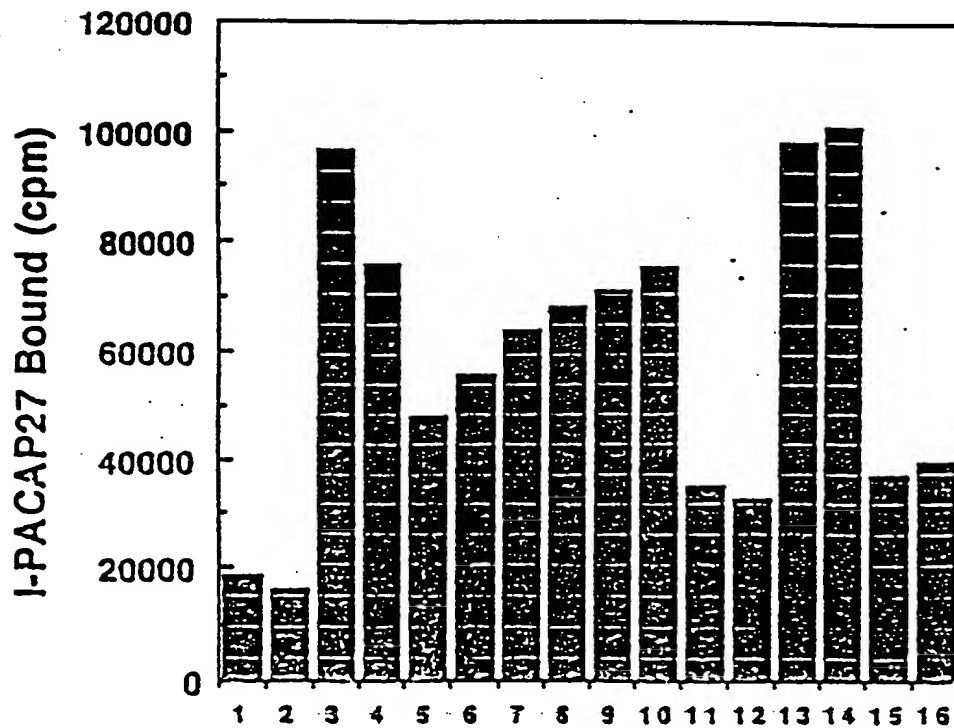


Fig. 43

No.

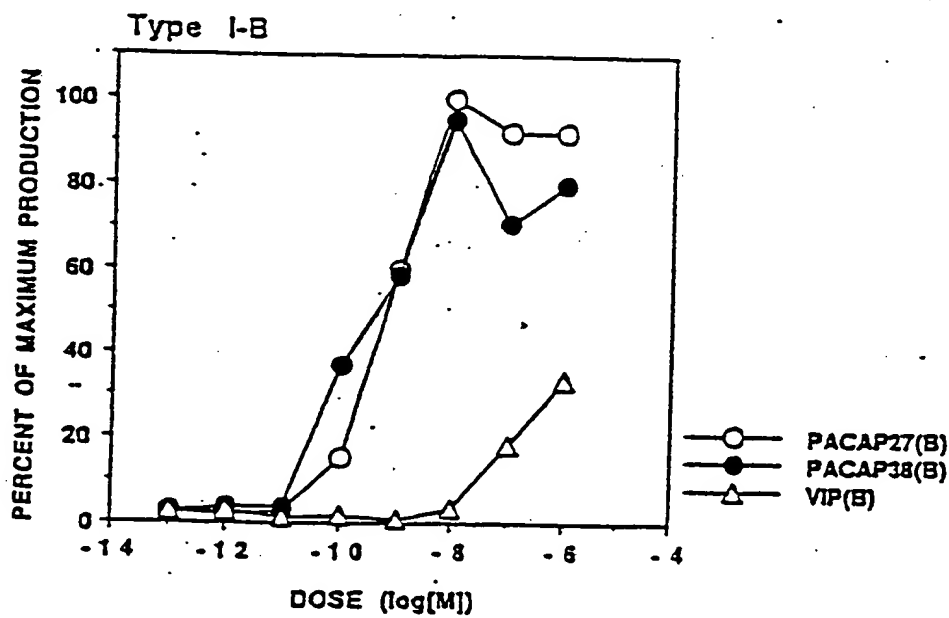
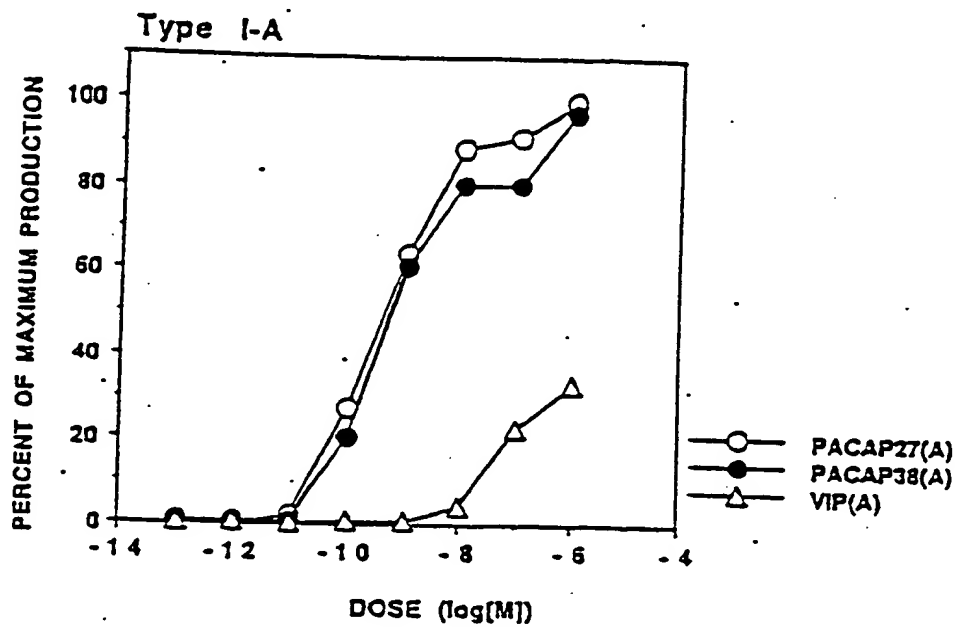


Fig. 44

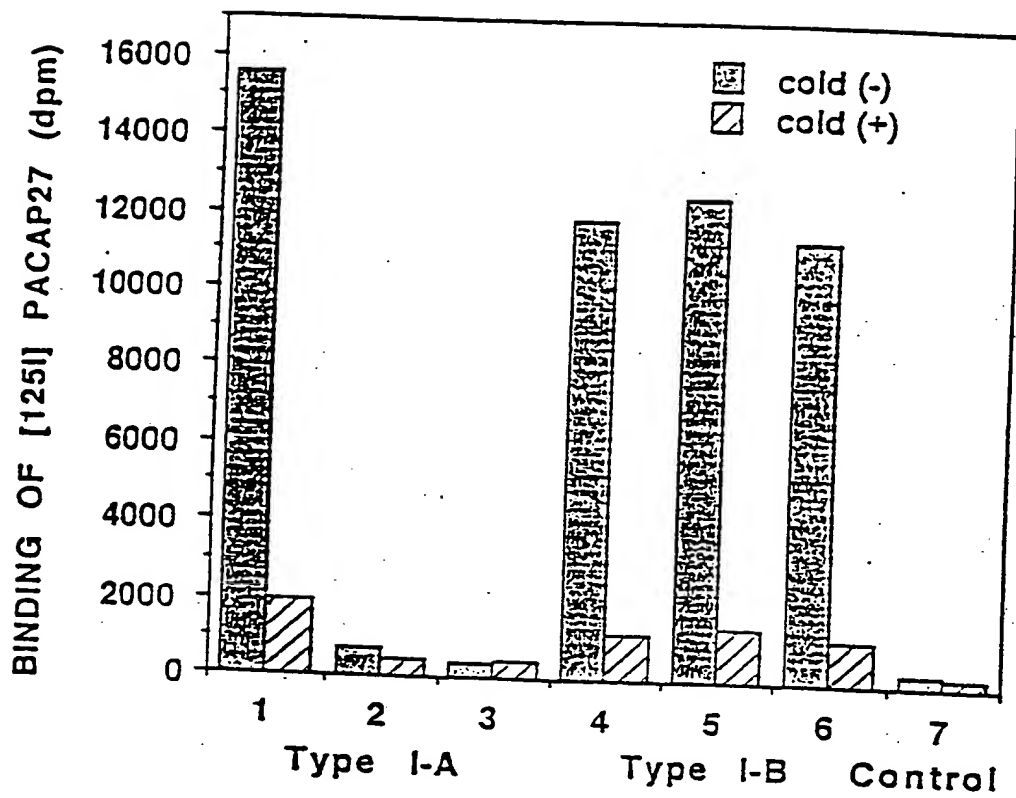
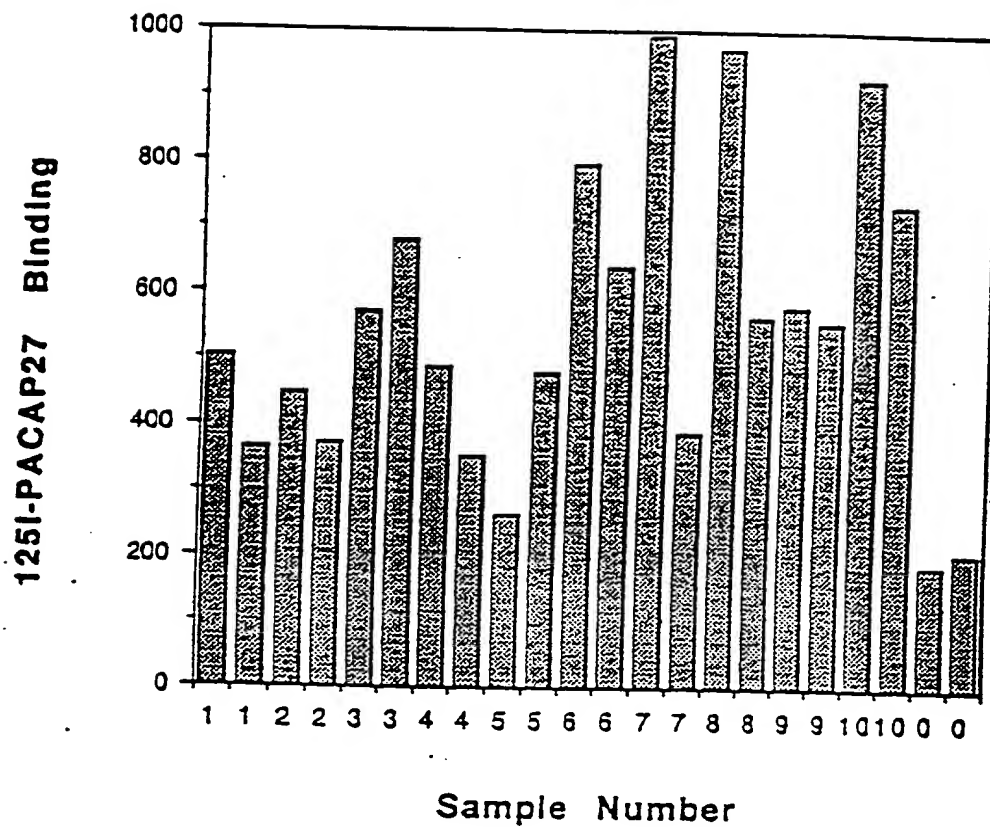


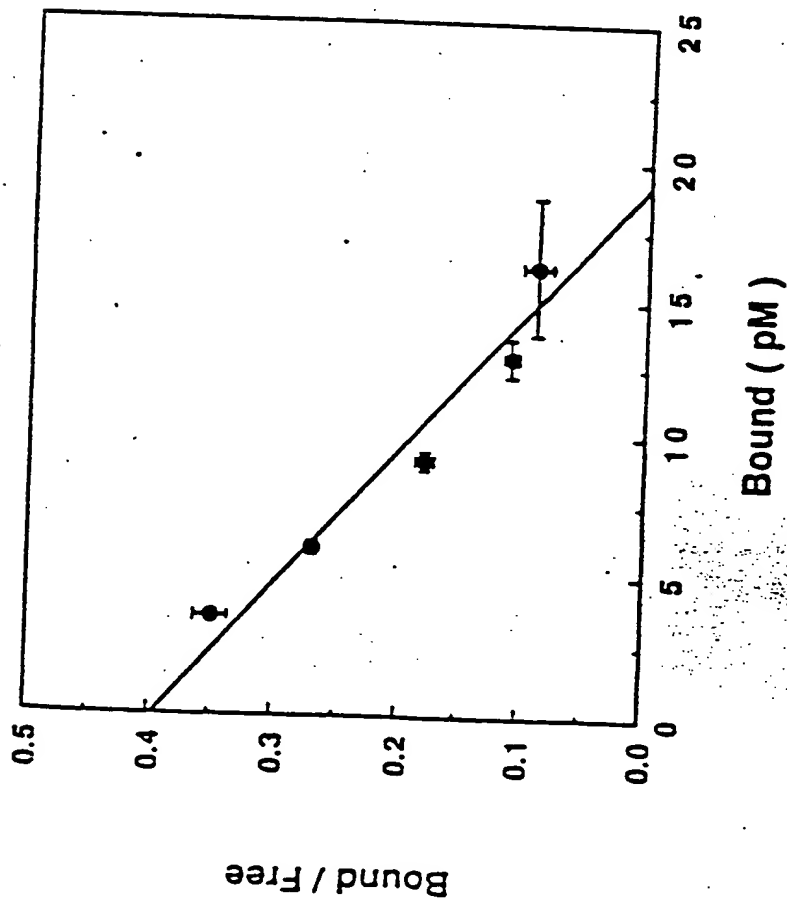
Fig. 45



FOUO 425669

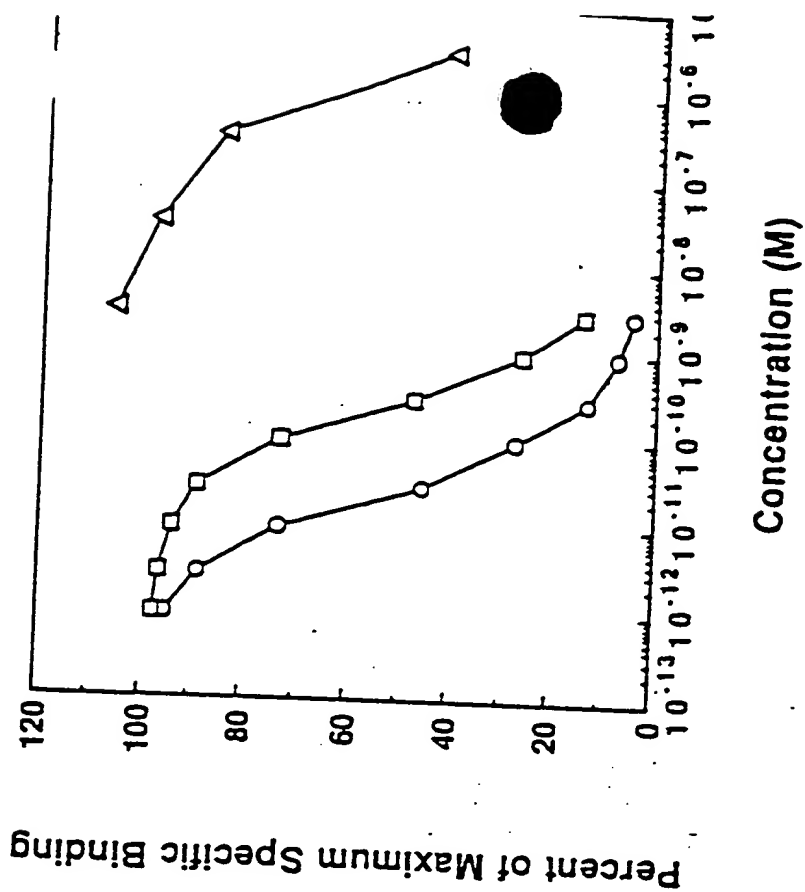
A

Fig. 46



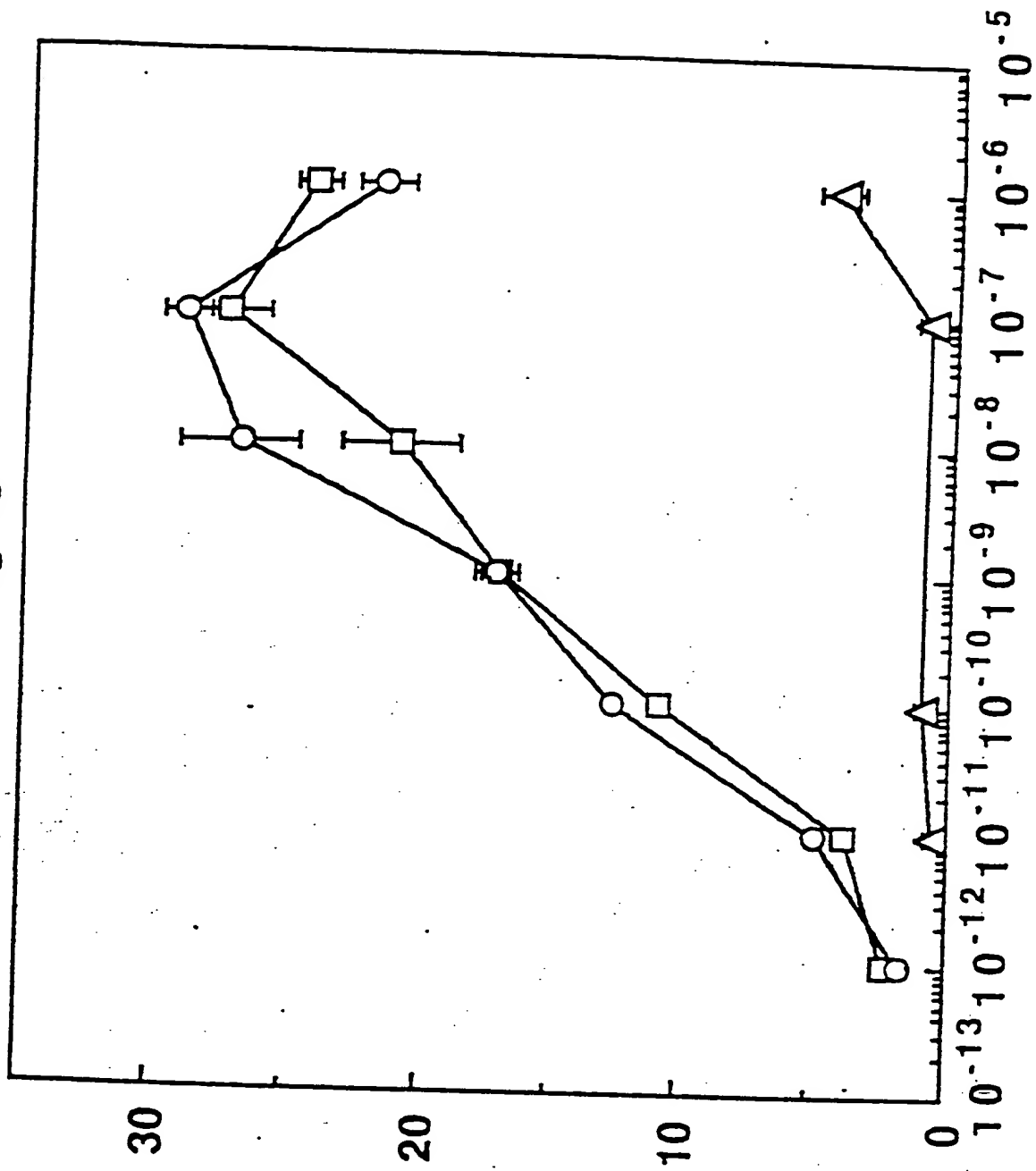
B

Fig. 47



Relative Content of Intracellular cAMP
(X control)

Fig. 48



Concentration (M)

Fig. 49

Brain
Lung
Liver
Thymus
Spleen
Pancreas
Placenta

(kb)

9.49 ↑
7.46 ↑
4.40 ↑
2.37 ↑
1.35 ↑
0.24 ↑



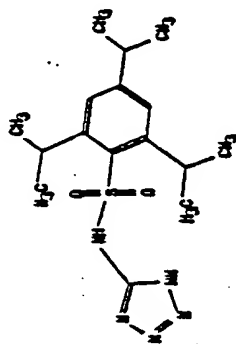
Fig. 50

Olfactory Bulb
Amygdala
Basal Ganglia
Hippocampus
Thalamus
Hypothalamus
Cerebral Cortex
Medulla
Cerebellum
Spinal Cord
Pituitary

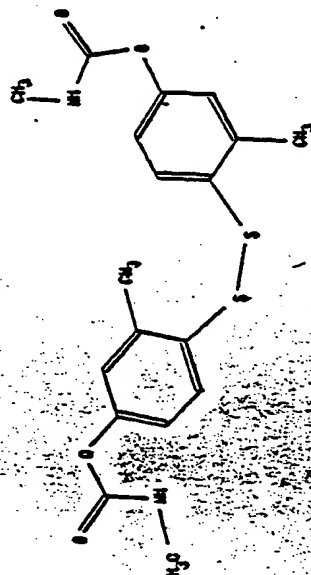
(kb)

9.49 ↑
7.46 ↑
4.40 ↑
2.37 ↑
1.35 ↑
0.24 ↑

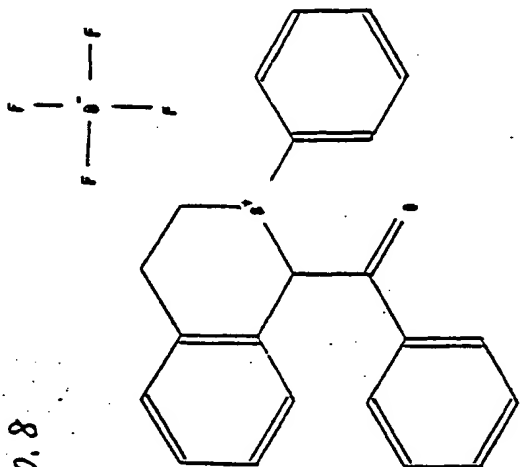




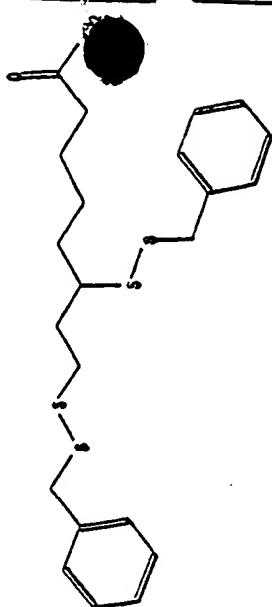
NO. 10



no. 8



110. 9



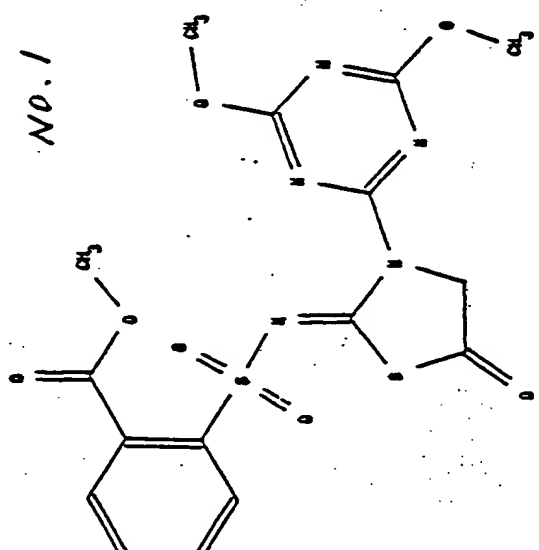
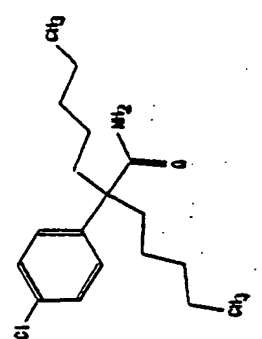
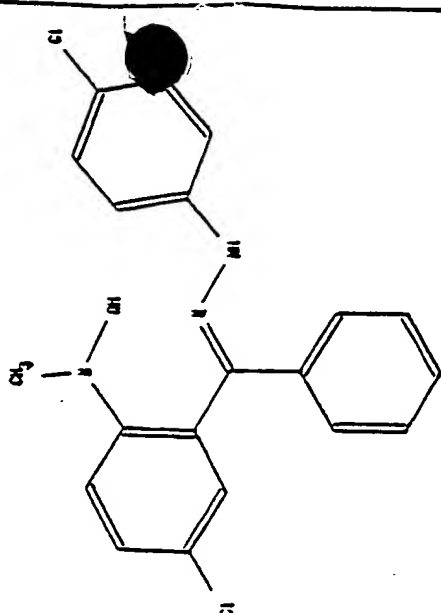
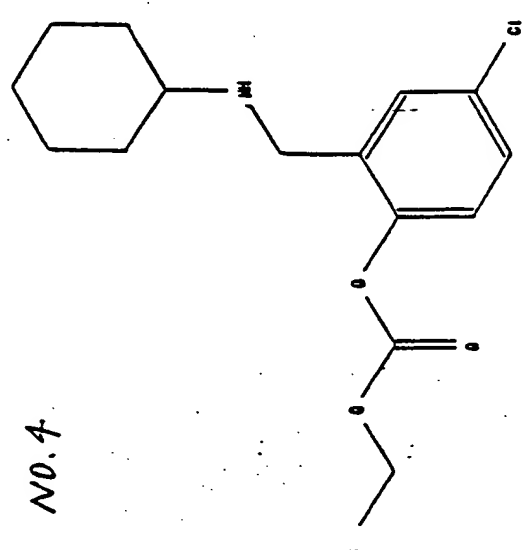
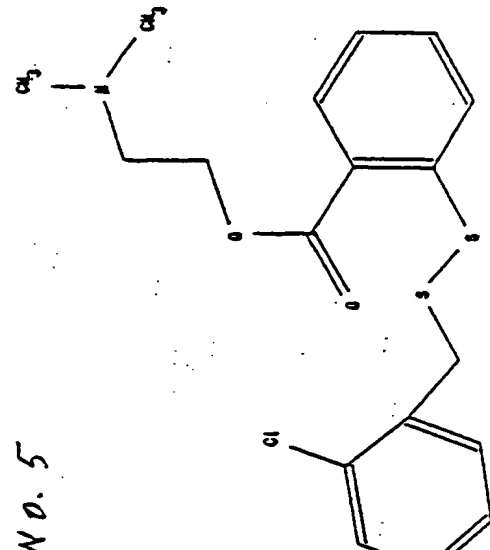
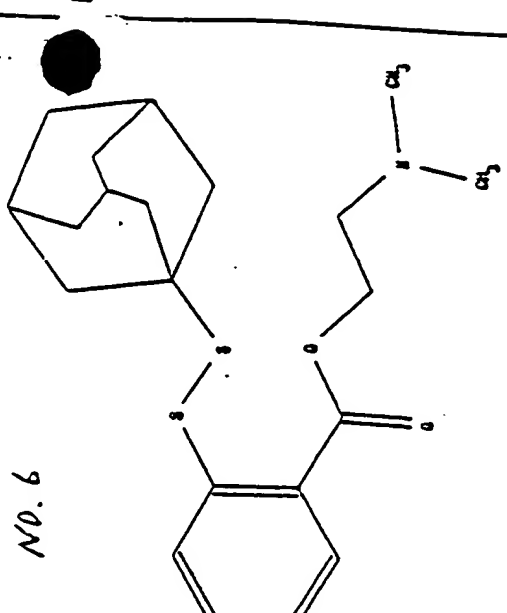
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<p>NO. 4</p> 	<p>NO. 5</p> 	<p>NO. 6</p> 

Fig. 52

A450

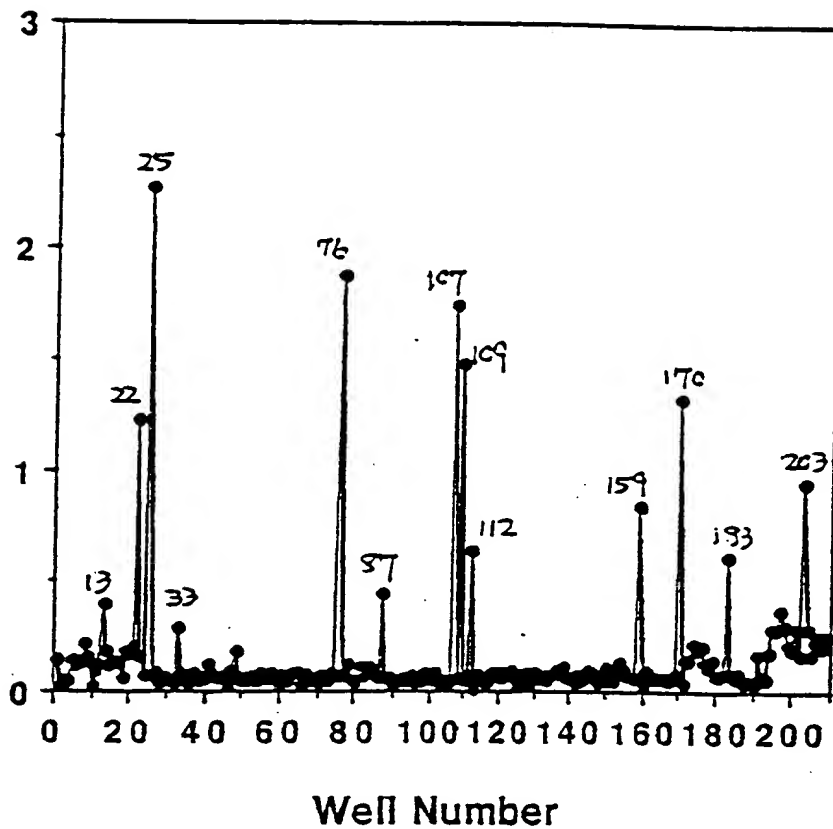


Fig. 53

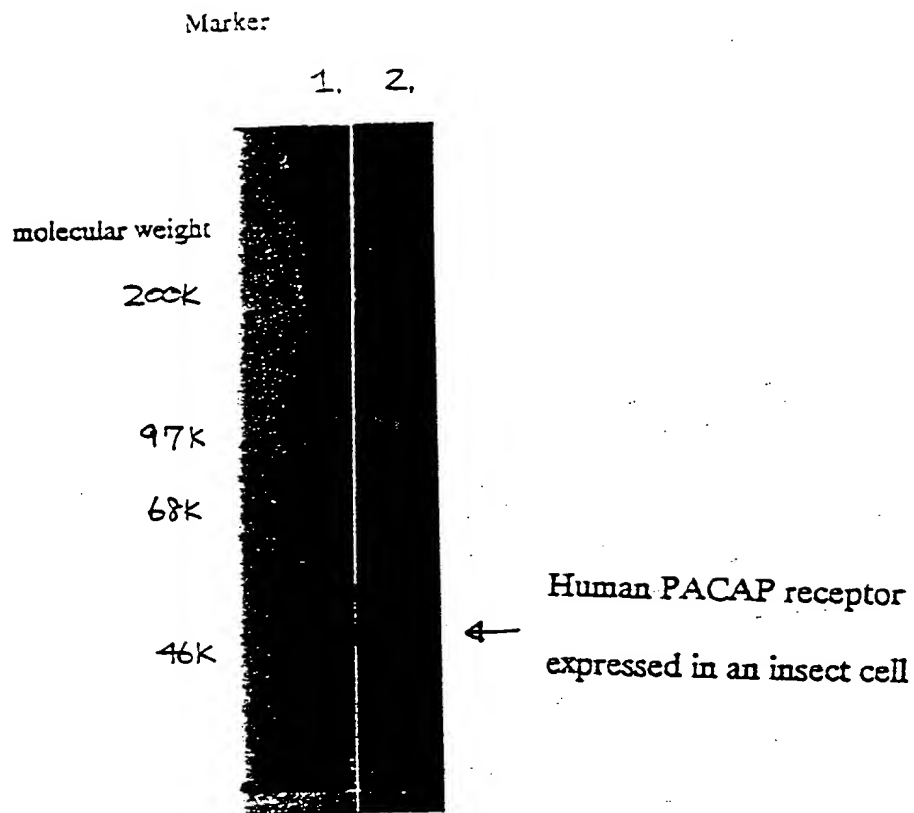


Fig. 54

